

97526

STIC-Biotech/ChemLib

From: Rao, Manjunath N.
Sent: Thursday, June 26, 2003 11:20 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search request for 09/762,767

Fr m: Manjunath N. Rao
Art Unit 1652, Room 10A11
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Phone: 306-5681

Date: 6-26-03

Please search the following as soon as possible for application with serial number **09/762,767**

1. SEQ ID NO:1 and 3, against all commercial nucleic acid databases including issued patents database and pending application database and provide a print of all results.
2. SEQ ID NO: 2 and 4 , against all commercial protein databases including issued patents database and pending application database and provide a print of all results.

If you have any questions please call me at the above phone number.

Thanks

Manjunath N. Rao, Ph.D.
Biotechnology Patent Examiner
Art Unit 1652, Room 10A11
Mail Box in 10D01
Crystal Mall 1, USPTO.

GenCore version 5.1.6
(c) 1993 - 2003 Compu

using sw model

```
3, 12:42:07 ; Search time 36.3713 Seconds
                (without alignments)
                2527.899 Million cell updates
```

7A-2
ITGECFSL.....QKKDVEDGNANFLGRASGID 690

Gapext 0.5

133250620 residues
 908470 chosen parameters:

00000

ch 0%
ch 100%
st 45 summaries

01002: *

[illegible]

er of results predicted by chance to have a value equal to the score of the result being printed is less than the total score distribution.

SUMMARIES

ID	Description
21	AA770475
21	AA751607
23	ABG61940
23	ABG61878
22	ABBS8042
21	AA751608
22	ABBS8149
22	ABBG0360
22	ABBS9684
22	AA883940

11	460	12.8	1025	14	AAR38863	GC-B. Rattus rattus
12	460	12.8	1047	12	AAAI03939	Human Natriluretic
13	460	12.8	1047	12	AAR10867	NPB(Pro655, Glu65
14	457.5	12.7	1029	13	AAR38862	GC-A. Rattus rattus
15	456.5	12.7	1061	23	AAU11280	Human atrionatriure
16	456.5	12.7	1061	23	AAU11281	Human atrionatriure
17	456.5	12.7	1075	22	AAU11783	Human ANP-A recept
18	456.5	12.7	1172	22	AAU812034	Drosophila melanog
19	453	12.6	1076	22	AB871206	Drosophila melanog
20	445	12.4	975	22	AB864661	Drosophila melanog
21	423.5	11.8	1525	22	AB871674	Drosophila melanog
22	421.5	11.7	566	22	AB861743	Drosophila melanog
23	408.5	11.4	887	22	ABG30657	Novel human diagn
24	408.5	11.4	1073	18	AAW32063	Novel human diagn
25	408.5	11.4	1073	19	AAW37371	Human ST receptor
26	408.5	11.4	1073	23	AAU087868	Human ST receptor
27	407.5	11.3	1075	14	AAR38861	Human guanylin cyc
28	403.5	11.2	1151	22	AAAB3939	GC-C. Rattus rattu
29	398.5	11.1	949	22	AAAB3941	Amino acid sequenc
30	397	11.0	669	22	AB865903	Amino acid sequenc
31	396	11.0	649	22	AB865902	Drosophila melanog
32	356	9.9	273	22	AAAG67400	Drosophila melanog
33	325.5	9.1	1077	22	AAU01924	Partial amino acid
34	325.5	9.0	1087	23	AAE14741	Human adenylate cy
35	325.5	9.0	1086	22	AAAD2938	Human adenylate cy
36	322.5	9.0	1086	23	AAE14742	Human adenylate cy
37	322	9.0	1064	21	AAAD2008	Human adenylate cy
38	319.5	8.9	1099	21	AAAD2011	Type IV adenylat
39	319	8.9	1090	17	AAAB94560	Type VII adenylat
40	319	8.9	1090	21	AAAB94560	Rat adenylat cycl
41	312	8.7	1086	23	AAE17129	Adenylat cyclase t
42	310.5	8.6	1103	23	AB811465	Human adenylat and
43	303.5	8.4	855	21	AB854358	Human adenylate cy
44	303.5	8.4	857	23	ABG54609	Human pancreatic c
45	303.5	8.4	857	23	ABG54609	Human albumin fusi
						Human gene 11 encod

ALIGNMENTS

RESULT 1
AAV70475
ID AAV70475 standard; Protein; 690 AA

04-JUL-2000 (first entry)

Human cyclic nucleotide-associated protein-3 (CNAP-3).

Cyclic nucleotide-associated protein-3; CNAP-3; human; cytosolic; anti-arteriosclerotic; hepatotropic; anti-leukemic; anti-inflammatory; immunomodulatory; anti-asthmatic; anti-naemic; anti-diabetic; diagnosis anti-sclerotic; dermatological; neuroprotective; anti-depressive; cancer; anti-Alzheimer's; anti-Parkinsonian; cerebroprotective; ophthalmological; anti-infertility; anti-allergic; vasotropic; immunosuppressive; hypotensive; gene therapy; prevention; treatment; arteriosclerosis; cell proliferative disorder; autoimmune/inflammatory; diabetes mellitus; neurological; vision; reproductive; smooth muscle.

OS	Homo sapiens.	
XX	Key	Location/Qualifiers
FT	Modified-site	65
FT	Modified-site	/note- "Potential phosphorylation site"
FT	Modified-site	211
FT	Modified-site	/note- "Potential phosphorylation site"
FT	Modified-site	361
FT	Modified-site	/note- "Potential phosphorylation site"
FT	Modified-site	450
FT	Modified-site	/note- "Potential phosphorylation site"
FT	Modified-site	478
FT	Modified-site	/note- "Potential phosphorylation site"

FT Modified-site 29 /note= "Potential phosphorylation site"
 FT Modified-site 73 /note= "Potential phosphorylation site"
 FT Modified-site 117 /note= "Potential phosphorylation site"
 FT Modified-site 135 /note= "Potential phosphorylation site"
 FT Modified-site 158 /note= "Potential phosphorylation site"
 FT Modified-site 229 /note= "Potential phosphorylation site"
 FT Modified-site 511 /note= "Potential phosphorylation site"
 FT Modified-site 527 /note= "Potential phosphorylation site"
 FT Modified-site 638 /note= "Potential phosphorylation site"
 FT Modified-site 687 /note= "Potential phosphorylation site"
 FT Modified-site 39 /note= "Potential phosphorylation site"
 FT Modified-site 64 /note= "Potential phosphorylation site"
 FT Modified-site 105 /note= "Potential phosphorylation site"
 FT Modified-site 261 /note= "Potential phosphorylation site"
 FT Modified-site 328 /note= "Potential phosphorylation site"
 FT Modified-site 356 /note= "Potential phosphorylation site"
 FT Modified-site 360 /note= "Potential phosphorylation site"
 FT Modified-site 394 /note= "Potential phosphorylation site"
 FT Modified-site 622 /note= "Potential phosphorylation site"
 FT Modified-site 635 /note= "Potential phosphorylation site"
 FT Modified-site 27 /note= "Potential phosphorylation site"
 FT Modified-site 332 /note= "N-glycosylated"
 FT Modified-site /note= "N-glycosylated"
 FT Modified-site 479 /note= "N-glycosylated"
 FT Modified-site 600 /note= "N-glycosylated"
 FT Modified-site 472..661 /note= "N-glycosylated"
 FT Region /note= "Guanylate cyclase signature sequence identified by PFAM analysis; CNAP-3 shares 89% identity with human, soluble guanylate cyclase large subunit"
 XX W0200014248-A1.
 PD 16-MAR-2000.
 PF 03-SEP-1999; 99WO-US20287.
 XX 04-SEP-1998; 98US-0148904.
 PA (INCY-) INCYTE PHARM INC.
 PI Hillman JL, Yue H, Guegler KJ, Corley NC, Patterson C, Tang YF.
 DR WPI: 2000-256994/22.
 DR N-PSDB: AAZ51684.
 XX Isolated cyclic nucleotide associated proteins useful for preventing, diagnosing and treating cell proliferative, autoimmune/inflammatory, neurological, vision, reproductive and smooth muscle disorders -
 XX

PS Disclosure: Page 67-69; 78pp; English.
 XX
 CC The present sequence is a human cyclic nucleotide
 CC associated protein-3 (CNAP-3), identified in incyte clone 159278,
 CC that is isolated from ADENINB01 cDNA library. It is expressed in
 CC nervous, reproductive, cardiovascular and developmental tissues.
 CC CNAP sequences may be used for prevention, treatment and diagnosis of
 CC diseases associated with altered CNAP expression such as, cell
 CC proliferative disorders (e.g. arteriosclerosis, cirrhosis, leukemia,
 CC lymphoma and cancer of the breast, prostate, lung and brain), autoimmune/
 CC inflammatory disorders (e.g. asthma, anemia, diabetes mellitus, multiple
 CC sclerosis and psoriasis), neurological disorders (e.g. epilepsy,
 CC Alzheimer's/Parinson's disease and strokes), vision disorders (e.g.
 CC conjunctivitis, glaucoma, cataracts and retinitis pigmentosa),
 CC reproductive disorders (e.g. infertility, uterine fibroids, ectopic
 CC pregnancies and impotence) and smooth muscle disorders (e.g. angina,
 CC anaphylactic shock, Keams-Sayre syndrome and hypertension). The
 CC coding sequence can be used for gene therapy.
 XX
 SQ Sequence 690 AA:
 Query Match 100.0%; Score 3593; DB 21; Length 690;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 MCTRLKDKLTGCEPFLAPGVNSESSEKATVPICDIEKNIQESLP 60
 1 MCTRLKDKLTGCEPFLAPGVNSESSEKATVPICDIEKNIQESLP 60
 61 QKTSRSRYVLTAESECKLFFPERLNVALQTLAKHKIKESKLEDEPKTAE 120
 61 QKTSRSRYVLTAESECKLFFPERLNVALQTLAKHKIKESKLEDEPKTAE 120
 121 QAVAGVVEVYKESIGEVEFKICEEDENILGVGTLKDFLNFSTILKSSHCQAG 180
 121 QAVAGVVEVYKESIGEVEFKICEEDENILGVGTLKDFLNFSTILKSSHCQAG 180
 181 KGRLEDAISICLQKEDDFLHYVYFPKRTSLIIPGIIKAAHYLYTEVEVSLMPCF 240
 181 KGRLEDAISICLQKEDDFLHYVYFPKRTSLIIPGIIKAAHYLYTEVEVSLMPCF 240
 241 HNDSEFVNOPYLAYSVMKSTKPSLSPKSSSVITPSECKTPEHFMEDMTLLQ 300
 241 HNDSEFVNOPYLAYSVMKSTKPSLSPKSSSVITPSECKTPEHFMEDMTLLQ 300
 301 FNGGIRRLANRRDPFGKPNFEVEFEIILPKINQTFSGIMTMNMQFVVRVRMDSYKS 360
 301 FNGGIRRLANRRDPFGKPNFEVEFEIILPKINQTFSGIMTMNMQFVVRVRMDSYKS 360
 361 SRVMDLKQMIYVSSAIIELVGSFCDRLDEFTGRGLYLSDIPIHNLRDVYLIGEQR 420
 361 SRVMDLKQMIYVSSAIIELVGSFCDRLDEFTGRGLYLSDIPIHNLRDVYLIGEQR 420
 421 AODGLKRLGKTKATLEBAHQALEBEKKRTVDLCSITPCVAAQDMQGVAAKKSNNV 480
 421 AODGLKRLGKTKATLEBAHQALEBEKKRTVDLCSITPCVAAQDMQGVAAKKSNNV 480
 481 TMLFSDIYGTALSCQSPLOYITMNLATYRFPDQCGELDYVKETGDAYCYAGGLHK 540
 481 TMLFSDIYGTALSCQSPLOYITMNLATYRFPDQCGELDYVKETGDAYCYAGGLHK 540
 541 ESDTHAVQIALMALKMELSDSVMSPHGEPIKMRIGLHSGSVFAGVGVKMPRYCLFGNN 600
 541 ESDTHAVQIALMALKMELSDSVMSPHGEPIKMRIGLHSGSVFAGVGVKMPRYCLFGNN 600
 601 VTINKFESCSVPRKINSPPTTYRLKDCPQFVTPRREELPPRPSBEIGICHFLDAY 660
 601 VTINKFESCSVPRKINSPPTTYRLKDCPQFVTPRREELPPRPSBEIGICHFLDAY 660
 661 OOGTNSKPCFQKDVEDGNANFLKASGID 690
 661 OOGTNSKPCFQKDVEDGNANFLKASGID 690

RESULT 2
AAV51607
ID AAV51607 standard; Protein: 690 AA.
XX
XX AAV51607;
XX
XX 26-MAY-2000 (first entry)
XX
XX Human soluble guanylyl cyclase alpha1 protein.
XX
XX Human: guanylyl cyclase alpha1; hsgcalpha1; hsgcbeta1; soluble;
XX guanylyl cyclase beta1; antiatherosclerotic; vasotropic; hypotensive;
XX gene therapy; arteriosclerosis; restenosis; ischemia; diagnosis;
XX peripheral arterial occlusive disease; arterial hypertension.
XX
XX Homo sapiens.
XX
XX DEL9837015-A1.
XX
XX 24-FEB-2000.
XX
XX 14-AUG-1998; 98DE-1037015.
XX
XX 14-AUG-1998; 98DE-1037015.
XX
XX (VASO-) VASOPHARM BIOTECH GMBH & CO KG.
XX
XX Schmidt H, Zabel U, Poller W;
XX
XX WPI, 2000-184044/17.
XX
XX N-PSDB; AA288938.
XX
XX New human soluble guanylate cyclase alpha1/beta1 and the nucleic acid
XX encoding the subunits, useful for producing diagnostic antibodies, and
XX for somatic gene therapy of arteriosclerosis -
XX
XX Example 1; Page 13-15; 44pp; German.
XX
XX This invention describes novel purified human soluble guanylate cyclase
XX alpha1/beta1 (hsgcalpha1/beta1). The products of the invention have
XX antiatherosclerotic, vasotropic and hypotensive activity. Nucleic acid
XX sequences encoding the alpha1 and/or beta1 subunit are useful for somatic
XX gene therapy of arteriosclerosis and restenosis, ischemia (infarct),
XX peripheral arterial occlusive disease and arterial hypertension.
XX Antibodies to hsgcalpha1/beta1 can be used for diagnosis of aberrant
XX hsgcalpha1/beta1 expression in human tissues. This sequence represents
XX the human soluble guanylyl cyclase alpha1 subunit described in the method
XX of the invention.
XX
XX Sequence 690 AA;
SQ
Query Match 100.0%; Score 3593; DB 21; Length 690;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 241 HNDCESEVNPYLLYSVHMASTKPSLSKPSQSLVPTSLFCKTFPHFMFDKMTILQ 300
QY 301 FGNIRRLMNRPOGKPNFEFEFEITLPKINOTFSGIMTMNMFVVRBRDMSYKKS 360
DB 301 FGNIRRLMNRPOGKPNFEFEFEITLPKINOTFSGIMTMNMFVVRBRDMSYKKS 360
QY 361 SRVMDLKGOMIYVESAILFELSPCYDRLEDFTRGLYLSIDIPINHALDVLIGBOAR 420
DB 361 SRVMDLKGOMIYVESAILFELSPCYDRLEDFTRGLYLSIDIPINHALDVLIGBOAR 420
QY 421 AOGGLKRLKLTATLEQAOALEEKKKIVDLCSIFPCVBAQMLQGVQAKKPSNV 480
DB 421 AOGGLKRLKLTATLEQAOALEEKKKIVDLCSIFPCVBAQMLQGVQAKKPSNV 480
QY 481 TMLFSDIVGFTALCSQSPLOVITMLNALYTRPDQCGELDYKVENTIGAYCAAGLHK 540
DB 481 TMLFSDIVGFTALCSQSPLOVITMLNALYTRPDQCGELDYKVENTIGAYCAAGLHK 540
QY 541 ESDTHAVQIALMALKMELESDVWSPHGEPIKMRIGLHSGSVFAGVGVKMPRYCLFGNN 600
DB 541 ESDTHAVQIALMALKMELESDVWSPHGEPIKMRIGLHSGSVFAGVGVKMPRYCLFGNN 600
QY 601 VTLANKFESCSVPKINVSPTTYRLKDCGCFVFTPPSRBELPPNPSEIPGICHFLDAY 660
DB 601 VTLANKFESCSVPKINVSPTTYRLKDCGCFVFTPPSRBELPPNPSEIPGICHFLDAY 660
QY 661 OOGTNSKPCFOKKDVEDGNANFLGKASGID 690
DB 661 OOGTNSKPCFOKKDVEDGNANFLGKASGID 690

RESULT 3
ABG61940
ID ABG61940 standard; Protein: 690 AA.
XX
XX ABG61940;
XX
XX 15-AUG-2002 (first entry)
XX
XX Prostate cancer-associated protein #141.
XX
XX Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.
XX
XX Mammalia.
XX
XX WO2002032068-A2.
XX
XX 18-APR-2002.
XX
XX 12-OCT-2001; 2001WO-US32045.
XX
XX 13-OCT-2000; 2000US-0687576.
XX 08-DEC-2000; 2000US-0733288.
XX 08-DEC-2000; 2000US-0733288.
XX 24-JAN-2001; 2001US-263957P.
XX 16-MAR-2001; 2001US-276791P.
XX 16-MAR-2001; 2001US-276888P.
XX 06-APR-2001; 2001US-281922P.
XX 24-APR-2001; 2001US-286214P.
XX 30-APR-2001; 2001US-0847046.
XX 04-MAY-2001; 2001US-288589P.
XX
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Glush KC, Mack DH, Wilson KE, Afar D, Hevezi P;
XX WPI, 2002-471335/50.
XX N-PSDB; ABK92259.
XX
XX Detecting a prostate cancer-associated transcript in a cell in a
XX patient, useful for diagnosing prostate cancer (PC) or screening
XX modulators of PC, by determining if prostate cancer-associated genes

are expressed in a prostate tissue -

Claim 27; Page 421-422; 436pp; English.

The present invention relates to methods of detecting a prostate cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer-associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer-associated genes are useful for diagnosing or treating prostate cancer, as well as for identifying modulators of prostate cancer or agents that inhibit prostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications.

ABG61800-ABG61944 represent prostate cancer-associated proteins.

Sequence 690 AA:

Query Match 100.0%; Score 3593; DB 23; Length 690;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MECTRLDKLKITGECFSLAPGVNPNSSSEAGSSSCATVPICODIPKNIQESLP 60
 1 MECTRLDKLKITGECFSLAPGVNPNSSSEAGSSSCATVPICODIPKNIQESLP 60
 61 ORKTSRSVYVYHTLAESTCKLFFPEERLNVALQTLAKHKIKESKSLERDEFTKTA 120
 61 ORKTSRSVYVYHTLAESTCKLFFPEERLNVALQTLAKHKIKESKSLERDEFTKTA 120
 121 QAVAGVVEVYKESIEEVEFKICEEDENILGVVGTGTLKDFLNFSTLLKSSCOENG 180
 121 QAVAGVVEVYKESIEEVEFKICEEDENILGVVGTGTLKDFLNFSTLLKSSCOENG 180
 121 QAVAGVVEVYKESIEEVEFKICEEDENILGVVGTGTLKDFLNFSTLLKSSCOENG 180
 181 KRGRLEDASTICLDKEDDFLHAYVFPKRTTSLIPGIIKAAHVLVEVEVSLMPDCE 240
 181 KRGRLEDASTICLDKEDDFLHAYVFPKRTTSLIPGIIKAAHVLVEVEVSLMPDCE 240
 241 HNDSEFVNOPYLLSYVHMKSTKPSLSKQSSSVITPSTLFCCKFPFHMDKMTLIQ 300
 241 HNDSEFVNOPYLLSYVHMKSTKPSLSKQSSSVITPSTLFCCKFPFHMDKMTLIQ 300
 241 HNDSEFVNOPYLLSYVHMKSTKPSLSKQSSSVITPSTLFCCKFPFHMDKMTLIQ 300
 301 FGNGIRRLANRRDFQGNFEEFEILPKINQTFSGIMTMNQFVVRVRMDSVKKS 360
 301 FGNGIRRLANRRDFQGNFEEFEILPKINQTFSGIMTMNQFVVRVRMDSVKKS 360
 301 FGNGIRRLANRRDFQGNFEEFEILPKINQTFSGIMTMNQFVVRVRMDSVKKS 360
 361 SRVMDLKQMTIYVSSAILEFGSPCVRLDEDFTRGLYLSDIPIHMLRDVYLIGEQAR 420
 361 SRVMDLKQMTIYVSSAILEFGSPCVRLDEDFTRGLYLSDIPIHMLRDVYLIGEQAR 420
 361 SRVMDLKQMTIYVSSAILEFGSPCVRLDEDFTRGLYLSDIPIHMLRDVYLIGEQAR 420
 421 AODGKRLGLTKATLEQAHALEBEKKRYVDLCSTPCFCAQOOLMGQVVAQAKFENV 480
 421 AODGKRLGLTKATLEQAHALEBEKKRYVDLCSTPCFCAQOOLMGQVVAQAKFENV 480
 421 AODGKRLGLTKATLEQAHALEBEKKRYVDLCSTPCFCAQOOLMGQVVAQAKFENV 480
 481 TMLPSDIYGFPAISQCSPLQVITMLNLYTRFDQCGELDYVKETIGDAYCVAGGLHK 540
 481 TMLPSDIYGFPAISQCSPLQVITMLNLYTRFDQCGELDYVKETIGDAYCVAGGLHK 540
 481 TMLPSDIYGFPAISQCSPLQVITMLNLYTRFDQCGELDYVKETIGDAYCVAGGLHK 540
 541 ESDTHAVOIALMALKMLSDVMSPHGEPIKMRIGLHSGSVFAGVGVKMDRYCLFGNN 600
 541 ESDTHAVOIALMALKMLSDVMSPHGEPIKMRIGLHSGSVFAGVGVKMDRYCLFGNN 600
 541 ESDTHAVOIALMALKMLSDVMSPHGEPIKMRIGLHSGSVFAGVGVKMDRYCLFGNN 600
 601 VTLANKFSSCVPRKINVSPTTYRLKDCRGVFPFRBRRELPRPFSEIIGICFLDAY 660
 601 VTLANKFSSCVPRKINVSPTTYRLKDCRGVFPFRBRRELPRPFSEIIGICFLDAY 660
 601 VTLANKFSSCVPRKINVSPTTYRLKDCRGVFPFRBRRELPRPFSEIIGICFLDAY 660
 661 QQGTNSKPCFOKRDVEDGNANFLGRASGID 690
 661 QQGTNSKPCFOKRDVEDGNANFLGRASGID 690

DB 661 QQGTNSKPCFOKRDVEDGNANFLGRASGID 690

RESULT 4
 ABG61878
 ID ABG61878 standard; Protein; 717 AA.
 XX
 XX ABG61878;
 AC
 XX
 XX 15-AUG-2002 (first entry)
 DT
 XX
 DE Prostate cancer-associated protein #79.
 XX
 XX Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.
 KM
 XX
 OS Mammalia.
 XX
 PN WO200230268-A2.
 PD
 XX 18-APR-2002.
 PE
 XX 12-OCT-2001; 2001WO-US32045.
 XX
 PR 13-OCT-2000; 2000US-0687576.
 PR 08-DEC-2000; 2000US-0733288.
 PR 08-DEC-2000; 2000US-0733742.
 PR 24-JAN-2001; 2001US-263957P.
 PR 16-MAR-2001; 2001US-276791P.
 PR 16-MAR-2001; 2001US-276888P.
 PR 06-APR-2001; 2001US-281922P.
 PR 24-APR-2001; 2001US-286214P.
 PR 30-APR-2001; 2001US-0847046.
 PR 04-MAY-2001; 2001US-288589P.
 PA
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 PI
 PI Gish KC, Mack DH, Wilson KE, Afar D, Hwezel P;
 DR
 DR WPI; 2002-471335/50.
 DR N-PSDB; ABK92193.
 XX
 PT
 PT Detecting a prostate cancer-associated transcript in a cell in a
 PT patient, useful for diagnosing prostate cancer (PC) or screening
 PT modulators of PC, by determining if prostate cancer-associated genes
 PT are expressed in a prostate tissue -
 XX
 PS
 PS Claim 27; Page 363; 436pp; English.
 CC
 CC The present invention relates to methods of detecting a prostate
 CC cancer-associated transcript in a cell from a patient. The method
 CC comprises contacting a biological sample from the patient with
 CC prostate cancer-associated polynucleotides (designated PC genes) that
 CC selectively hybridise to a sequence that is at least 80% identical
 CC to them. The prostate cancer-associated polynucleotide sequences
 CC are differentially expressed in prostate tumour tissue or in
 CC prostate cancer and are derived from the tissues of various
 CC organisms such as humans or other mammals (e.g. mice, sheep and dogs).
 CC The methods of the invention are useful for diagnosing and treating
 CC prostate cancer in mammals. The prostate cancer-associated genes are
 CC useful for diagnosing or treating prostate cancer, as well as for
 CC identifying modulators of prostate cancer or agents that inhibit
 CC prostate cancer. The nucleic acid sequences are particularly useful
 CC in gene therapy, as a vaccine or in antisense applications.
 CC ABG61800-ABG61944 represent prostate cancer-associated proteins.
 CC
 XX
 SO
 SO Sequence 717 AA:

Query Match 88.3%; Score 3171.5; DB 23; Length 717;
 Best Local Similarity 90.7%; Pred. No. 11e-294;
 Matches 625; Conservative 10; Mismatches 37; Indels 17; Gaps 4;

1 MECTRLDKLKITGECFSLAPGVNPNSSSEAGSSSCATVPICODIPKNIQESLP 60
 1 MECTRLDKLKITGECFSLAPGVNPNSSSEAGSSSCATVPICODIPKNIQESLP 60
 1 MECTRLDKLKITGECFSLAPGVNPNSSSEAGSSSCATVPICODIPKNIQESLP 60

```

Db      1 MECTKAKDKITGCEPFLIAPGQVNESSEAAAGSESCATVPICQDIPERNQIESLP 60
QY      61 ORKTSRVRVYLTHTLAESICKLIPPEPERLVALQRLAKHKIKESKSLEREDFEKTIAT 120
Db      61 ORKTSRVRVYLTHTLAESICKLIPPEPERLVALQRLAKHKIKESKSLEREDFEKTIAT 120
QY      121 QAVAGVPEVAVIKESIGEVEFKICYEDENILGAVGGTAKDFINSEFTLLKQSSHCQE-- 178
Db      121 QAVAGVPEVAVIKESIGEVEFKICYEDENILGAVGGTAKDFINSEFTLLKQSSHCQE-- 178
QY      179 -----AGKRGRLDASITLCLDKEDDLHYVYFPPKRTTSLILPGITAKAAHYVYEVYEV 233
Db      172 QRLPRKRRKGQLDASITLCLDKEDDLHYVYFPPKRTTSLILPGITAKAAHYVYEVYEV 231
QY      234 SLMPPCFHNDCSEFVQPYLLYSVHAKSKTKPSLSPKPOSSIVIPISLFCPTPPFHPMD 293
Db      232 SLMPPCFHNDCSEFVQPYLLYSVHAKSKTKPSLSPKPOSSIVIPISLFCPTPPFHPMD 291
QY      294 KDMTILQFNGIRRLNRRDPQCKPNEFEYFEILTPKINQTFESGIMTMLMNOFVAVRVM 353
Db      292 KDMTILQFNGIRRLNRRDPQCKPNEFEYFEILTPKINQTFESGIMTMLMNOFVAVRVM 350
QY      354 DNSVKSRRVMDLKGOMIYIVESSALIFGSPCVDLDPDTGGLYLSQIPHNALRDVY 413
Db      351 DNSVKSRRVMDLKGOMIYIVESSALIFGSPCVDLDPDTGGLYLSQIPHNALRDVY 410
QY      414 LIGEQARADGKLKRRGKTLKATLEQAHQALEEKKKTVDLCSIFPCVQAQQLMOGOVYQ 473
Db      411 LIGEQARADGKLKRRGKTLKATLEQAHQALEEKKKTVDLCSIFPCVQAQQLMOGOVYQ 470
QY      474 AKKFSVNTMLFSDIVGFTAIQSCSPLOYITMLNLYTRFDQCCGGLDLYKVTETIGDAYC 533
Db      471 AKKFSVNTMLFSDIVGFTAIQSCSPLOYITMLNLYTRFDQCCGGLDLYKVTETIGDAYC 530
QY      534 VAGGLKESDTHAVOIALAKMMEISDEVMSPHGPBKIRIGLHSGSVAGVYKMPR 593
Db      531 VAGGLKESDTHAVOIALAKMMEISDEVMSPHGPBKIRIGLHSGSVAGVYKMPR 590
QY      594 YCLFGNNVTLANKFESCSVPKINVSPTTYRLKDCPGFVTPRSREBELPNNPSEIPIGI 653
Db      591 YCLFGNNVTLANKFESCSVPKINVSPTTYRLKDCPGFVTPRSREBELPNNPSEIPIGI 650
QY      654 CHEFLAYQOGTNSKPCFOKKVDGNAHF 682
Db      651 CHEFLAYQOGTNSKPCFOKKVDGNAHF 679

```

RESULT 5
ABBS8042
ID .ABBS8042 standard; Protein; 676 AA.

```

XX AC ABBS8042;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 918.
XX KM Drosophila; developmental biology; cell signalling; insecticide;
XX KM pharmaceutical.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001MO-US09231.
XX PR 23-MAR-2000; 2000US-191637P.
XX PR 11-JUL-2000; 2000US-0614150.
XX PA (PEKE ) PE CORP NY.

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PI Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
DR N-PSDB; AB102145.
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX Disclosure; SEQ ID NO 918; 21np + Sequence Listing; English.
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB11840-AB11675) and the encoded proteins
CC sequences (AB101840-AB11675) and the encoded proteins
CC (ABBS7737-ABBS7072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 676 AA:
SQ
Query Match 27.6%; Score 991.5; DB 22; Length 676;
Best Local Similarity 37.8%; Pred. No. 1,3e-85;
Matches 247; Conservative 117; Mismatches 209; Indels 81; Gaps 20;
QY 58 SLPORTSRVRVYLTHTLAESICKLIPPEPERLVALQRLAK-----HKIK---ESR 106
Db 27 ALDEDEELSDALTLHLQALQIQLTAPSNEDLTAVTSIAKYRQMPNHIKIKLDPQTE 86
QY 107 KSLERDEFEKTIAE-----QAVAGVPEVAVIKESIGEVEFKICYER-DENILGVCGLT 159
Db 87 KSCANTDYLDLDELKIKDASASELTV-----LASEELITCCGIGIIRAFRCIGTDL 141
QY 160 KDEFLNSES---TLKQSSHCQEAQKRGRLDASITLCLDKEDDLHYVYFPPKRTTSLILP 216
Db 142 QEFLGLSDGYDVIAK---LQEDD---VYDTGVCAGGEE---LFTSERVYIMLL 189
QY 217 GITKAAAHVYEVYEVYSLMPPCFHNDCSEFVQPYLLYSVH-----MKSTKP-SUSPSK 270
Db 190 GSKALTRMLKYDVNIKIEP--VEGDARRY---RYFLSVLYKQNSOTMLGRPTYSKTI 244
QY 271 PQ-----SSIVIPISLFCPTPPFHPMDKMTILQFNGIRRLNRRDPQCKPNE 320
Db 245 PETVQNSNSMASDLOANNSSFCMKPFMHITNDELVELVQKGFSLY-----KPYM 297
QY 321 EE-----YFEILTPK-INQTFSGIMTMLMNOFVAVRVMDSVYKSSRVMDLKGOMIY 372
Db 298 ADFGCGATYFDFKRRPGGLMKFRDIYRRTYTFEFLGLNPPGAVNDPAIGLEIKGMVH 357
QY 373 TVESSALIFGSPCVDLDPDTGGLYLSQIPHNALRDVYLIGEQARADGKLKRRGKTL 432
Db 358 CPESNSLIFGSPFLDGLTCLNGLEISDIPHDATREYIIVGEQARADGKLRRRMDKI 417
QY 433 KATLEQAHQALEEKKKTVDLCSIFPCVQAQQLMOGOVYQAKKFSVNTMLFSDIVGFTA 492
Db 418 KNSIEEANSVYTERKKNVSLHLIPPAETAEKMLGSSSIDATYTPVITLLESDIVGFTS 477
QY 493 ICSQSPLOYITMLNLYTRFDQCCGGLDLYKVTETIGDAYCVAGGLKESDTHAVOIALM 552
Db 478 ICSRAPFPVVISMLGKDFDECDPFDYKYKVTETIGDAYCVAGGLHRASTIDAHKAYAM 537
QY 553 ALKAMEISDEVMSPHGPBKIRIGLHSGSVAGVYKMPRCLFGNNVTLANKFESCSV 612
Db 538 ALKMDIACSKHITHDEQIKMRIGLHGTGLAGVYKMPRCLFGHSTVIANKFESGSE 597
QY 613 PKRINVSPTTYRLKDCPGFVF--TPRSREBELPNNPSEIPIG--ICHPIDAVO 661
Db 598 ALKINVSPTTKDMITKHEGFEEFLQRPDSFLLKREPPN--PGGTETCYFLESFR 649

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OY 638 SREELP-----PMPSEIPGICHELDAVOGNTS 666
 DB 595 RENNRLPDLTALQVHPLSPS-----HLLPRDLQGGCS 627

RESULT 9

ABB59684
 ID ABB59684 standard; Protein; 1076 AA.

XX ABB59684;

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 5844.

XX Drosophila: developmental biology; cell signalling; insecticide;

XX pharmaceutical.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.

XX 23-MAR-2000; 2000US-191637P.

XX 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI, 2001-656860/75.

XX N-PSDB; ABL03787.

XX New isolated nucleic acid detection reagent for detecting 1000 or more

XX genes from Drosophila and for elucidating cell signalling and cell-cell

XX interactions -

XX Disclosure; SEQ ID NO 5844; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent

XX capable of detecting 1000 or more genes from Drosophila. The invention is

XX useful in developmental biology and in elucidating cell signalling and

XX cell-cell interactions in higher eukaryotes for the development of

XX insecticides, therapeutics and pharmaceutical drugs. The invention

XX discloses genomic DNA sequences (AB16176-AB130511), expressed DNA

XX sequences (AB101840-AB16175) and the encoded proteins

XX (ABB57737-ABB72072).

XX The sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format directly from WIPO

XX at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1076 AA;

Query Match 12.9%; Score 462; DB 22; Length 1076;

Best Local Similarity 43.6%; Pred. No. 1.7e-34;

Matches 109; Conservative 38; Mismatches 91; Indels 12; Gaps 5;

OY 404 PIHNAIRD---VLLIGEQARAQDGLKRRL---GRLKATLEQAHALEEEKKTVDLCS 456

DB 785 PTFSTIRBNIRITIMKPCENLMDLLNMEQYANLLESLVEKTKQLSLEKQRTLELLXQ 844

OY 457 IFPCVAAQOLMOGOVVOAKKFSNVTMLFSDIVGFTAGSCSPLOVITMLNALYTRFDQO 516

DB 845 ILPRVAAQOLMAGDLYDEEFSSTVITYFSDIVGFTLECARSSPMOVNMLNDLYSTFDR 904

OY 517 CGELDYVYVETLTGAAYCAAGC-HKESPTHAVOIALMKMELSDVMSRGEF---IK 572

DB 905 IGFYDYVYVETLTGAAYCAAGC-HKESPTHAVOIALMKMELSDVMSRGEF---IK 572

OY 573 MRIGHSVSFAGVGVAMPKRYCLGNNVTLANKFESCVPRKINVSPTTYRLKDCPGF 632

DB 964 INIGHSSSVACAGVGVKMKPHICLFGDTVNTASRMESTGQPKIHVSATFALLDKFGTF 1023
 OY 633 VFTPRSREL 642
 DB 1024 QMEGRGDVEL 1033

RESULT 10

AAB83940
 ID AAB83940 standard; Protein; 1115 AA.

XX AAB83940;

XX 23-JUL-2001 (first entry)

XX Amino acid sequence of a guanylyl cyclase-2 chemoreceptor (HG-gcy-2).

XX Soybean cyst nematode; guanylyl cyclase-1 chemoreceptor; HG-gcy-1;

XX parasitic nematode; chemotaxis; HG-gcy-2.

XX Heterodera glycines.

XX WO200134791-A2.

XX 17-MAY-2001.

XX 02-NOV-2000; 2000WO-US30295.

XX 05-NOV-1999; 99US-0435376.

XX (UNYC-) UNIV NORTH CAROLINA STATE.

XX Davis EL, Yan Y;

XX WPI, 2001-335924/35.

XX N-PSDB; AAF89878.

XX Novel isolated polynucleotide encoding nematode guanylyl cyclase

XX chemoreceptor, useful for controlling plant feeding nematodes -

XX Example 2; Page 55-59; 69pp; English.

XX The present sequence represents soybean cyst nematode guanylyl cyclase-2

XX chemoreceptor, designated HG-gcy-2. HG-gcy-1 polynucleotides and

XX polypeptides are useful as active agents for controlling plant

XX feeding nematodes. They can be used to screen for compounds that have

XX the ability to disrupt parasitic nematode feeding or chemotaxis.

XX Sequence 1115 AA;

Query Match 12.8%; Score 461; DB 22; Length 1115;

Best Local Similarity 40.6%; Pred. No. 2.2e-34;

Matches 114; Conservative 38; Mismatches 101; Indels 28; Gaps 6;

OY 376 SSAIFLGSPCVD-----RLDEFTGRLVLSIDPIHNAIRDVYLIGEQAADGLKRR 428

DB 812 SPALHLHLTKKDWSDSPAPRPKMEYV-----ALLQSNMGRSTNMLDHYFNM 858

OY 429 L-----GRLKATLEQAHALEEEKKTVDLCSIFPCVAAQOLMOGOVVOAKKFSNVTMLF 484

DB 859 LEVYAGSLSEEEVEERTKELVEKKTDLILYRMLPKQVADLTKLQGSVEPETFCYVYF 918

OY 485 SDIVGFTAGSCSPLOVITMLNALYTRFDQOCEGLDYVYVETLTGAAYCAAGC-HKESD 543

DB 919 SDVVSFTTIAKSCSPLOVITMLNALYTRFDQOCEGLDYVYVETLTGAAYCAAGC-HKESD 978

OY 544 THAVOIALMKMELSDVMSRPH--GEPIMRIGHSVSFAGVGVAMPKRYCLGPGNNV 601

DB 979 EHAQHIAKMSLAFNMKISFTPIHLPIERLRLRIGIHGSGTVAGVGLSMBRYCLFGPTI 1038

OY 602 TLANKFESCVPRKINVSPTTYRLKDCPGFVFTPRSREL 642

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Db      1039  NTAARLESSSKPMRIHISTTNHFLVNNVIG-GFTVQANGEL 1078
RESULT 11
ID      AAR38863
AC      AAR38863;
DT      08-FEB-1994 (first entry)
DE      GC-B.
KW      Guanylyl cyclase; GC-C; heat stable; enterotoxin; rat; small intestine;
        mucosa; polyA+ RNA; PCR; enterotoxin receptor; bacterial enterotoxin;
        binding domain; antibody; diarrhoea; ligand; antagonist.
OS      Rattus rattus.
XX      US5237051-A.
XX      17-AUG-1993.
XX      06-DEC-1990; 90US-0623033.
XX      06-DEC-1990; 90US-0623033.
XX      06-DEC-1990; 90US-0623033.
XX      (UYVA-) UNIV VANDERBILT.
XX      PA
XX      Garbers DL, Schulz S;
XX      WPI; 1993-272183/34.
XX      New purified enterotoxin receptor protein - used to develop
XX      PT prods. for treating abnormal conditions caused by bacterially
XX      PT released enterotoxin, partic. diarrhoea
XX      Disclosure; Fig 3; 26pp; English.
XX      PS
XX      The sequences given in AAR38862-63 represent the guanylyl cyclases,
XX      CC GC-A and GC-B, which binds heat stable enterotoxin. These proteins
XX      CC are enterotoxin receptors which may be used as a therapeutic to control
XX      CC intestinal fluid permeation as well as abnormal conditions caused
XX      CC by bacterially released enterotoxin. The binding domain of the
XX      CC proteins, or antibodies to the proteins, can be used to eliminate
XX      CC diarrhoea. The proteins may be used to isolate ligands and to screen
XX      CC for antagonists of toxin binding. This sequence is given as it is
XX      CC represented in the specification.
XX      SQ
Sequence 1025 AA;
Query Match 12.8%; Score 460; DB 14; Length 1025;
Best Local Similarity 41.9%; Pred. No. 2,4e-34;
Matches 113; Conservative 39; Mismatches 76; Indels 42; Gaps 6
QY      411 DVLVIGEARAD-----GLKRRK-----LKATLBOA 439
Db      738 ELVLIMERCMAQDPTERDFGQIKGFIIRFNKEGTSILDNLLEMQYANLKEKTVBER 797
QY      440 HQALEEEKKRVNDDLCSTFPEVNAQOLMGQGVQAKKRSNTMLFSDIVGFAICSCQSP 499
Db      798 TQATLEERKKKDALYQLPLPSVAEQKRGTEVQAEDSVATYFSDIVGFTALSAESTP 857
QY      500 LQVITMLNALATRFDOQCGELDYVKVETIGDAYCVAAGL-HRESPTHAVQATMLAKMME 558
Db      858 MQVYTLNLNDLYTCEDATIDNEDYKIVETIGDAYVWVSGLPGRNGQRHAPETARALALL- 916
QY      559 LSDEYMS-----DHGEIKMRIGLHSGSVAGVGVKMPRYCLFGNNVTLANKEQSCSV 612
Db      917 --DAVSSPRIRHRRPL-DQLRLRIQVHTGTPVCAGVYGLMKPRYCLFGDVTNVAASRMSGQ 973
QY      613 PKRTINVSPTTYRLKDCRGFFVTRSRREL 642

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Db	974	ALKIHVSSTTKMALDELGCFOLELRDVM	1003
RESULT 12			
AA10399			
ID	AA10399	standard; Protein; 1047 AA.	
AC	AA10399;		
XX			
DT	09-APR-1991	(first entry)	
XX			
DE	Human Natriuretic Peptide Receptor B.		
XX			
KW	NPBR; ANP; BNP; CND; kidney failure; heart failure; protein kinase;		
RW	hyperaldosteronism; glaucoma; guanyl cyclase.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Peptide	1..22	
FT		/label= signal sequence	
FT	Protein	12	
FT		/label= mature NPBR	
FT	Domain	23..455	
FT		/label= extracellular domain	
FT		/note= "binds natriuretic peptides A,B and C".	
FT	Domain	456..456	
FT		/label= transmembrane domain	
FT	Domain	479..1047	
FT		/label= cytoplasmic domain	
FT		/note= "Gc and protein kinase activity"	
FT	Modified-site	24..26	
FT		/label= N-glycos_site	
FT	Modified-site	35..37	
FT		/label= N-glycos_site	
FT	Modified-site	161..163	
FT		/label= N-glycos_site	
FT	Modified-site	195..197	
FT		/label= N-glycos_site	
FT	Modified-site	244..246	
FT		/label= N-glycos_site	
FT	Modified-site	277..279	
FT		/label= N-glycos_site	
FT	Modified-site	349..351	
FT		/label= N-glycos_site	
FT	Modified-site	600..602	
FT		/label= N-glycos_site	
XX			
PN	W09100292-A.		
XX			
PD	10-JAN-1991.		
XX			
PE	22-JUN-1990;	90WO-US03586.	
XX			
PR	23-JUN-1989;	89US-0370673.	
XX			
PA	(GETH) GENENTECH INC.		
PI	Chang M, Goeddel D, Lowe D;		
XX			
DR	WPI; 1991-036711/05.		
DR	N-PSDB; AAQ10324.		
XX			
PT	Natriuretic protein receptor B - for diagnosis and treatment of		
XX	kidney failure, heart failure, hyperaldosteronism, glaucoma etc.		
PS	Claim 3; Fig 1; 49pp; English.		
XX			
The sequence was derived from the DNA encoding natriuretic peptide receptor B, NPBR, having guanylyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the prodn. of the protein, opt. after being mutated to produce NPBR analogues. The protein has a mol wt. of 115 kD (calculated Mr			

CC 114,952). The protein (or variants) can be used in treatment of
 CC natriuretic peptide disorders, and also to isolate peptides using
 CC affinity chromatography. Antibodies with affinity for NPRB can
 CC also be prep'd. An analogue, NPRBDC, comprising only AAs 1-433 of
 CC the mature protein, is also claimed, as well as variant described
 CC in AAR10867.

XX Sequence 1047 AA;

Query Match 12.8%; Score 460; DB 12; Length 1047;
 Best Local Similarity 41.9%; Pred. No. 2.5e-34;
 Matches 113; Conservative 39; Mismatches 76; Indels 42; Gaps 6;

QY 411 DVTLIGEARAD-----GLKRLGK-----LKAATLEQA 439
 DB 760 ELVLLMERCWADPAERPDFOGIRFRFKEGSTILDMLLRMEQYANLEKIVEER 819
 QY 440 HQALEEKKKTVDLICSFPCVAAQOLMGQVQAKKSNVTMLFSDIVGFAISCQSP 499
 DB 820 TQATLEERKKAALYQILPHSVAEQLRGETVQAEADSVITFSYDVGFTALSAESTP 879
 QY 500 LQVITMLNALTFRDQCGELDYKVEITGDAYCAGGL-HKESDTHAVQIALMKME 558
 DB 880 MQVTLNLDLYTCEDAIIDNFDYKVEITGDAYVWSGLPGRNGORHAPETARALALL- 938
 QY 559 LSDEYMS-----PHGEPIKRIKIGHSVFAGVGVMPRYCLFGNNVTIANFESCSV 612
 DB 939 --DAVSSFRIRHPR-DQLRLRIGVHTGVCAGVGLKMPRYCLFGDVTNASHMESNGQ 995
 QY 613 PRKINVSPTTYRLKDCGPFVTPRSREEL 642
 DB 996 AKTIHVSSTKDALDELGCFOLELRGDYEM 1025

RESULT 13

AAR10867
 ID AAR10867 standard; Protein; 1047 AA.

XX AAR10867;
 XX 09-APR-1991 (first entry)
 XX NPBR(Pro655, Glu656, Leu663, Phe664, Ala682).
 XX NPBR; ANP; BNP; kidney failure; heart failure; protein kinase;
 XX hyperaldosteronism; glaucoma; guanyl cyclase.
 XX Homo sapiens.
 PH Key
 FT Peptide 1..22 Location/Qualifiers
 FT /label= signal sequence
 FT Protein 12
 FT /label= mature NPBR
 FT Domain 23..455
 FT /label= extracellular domain
 FT /note= "binds natriuretic peptides A, B and C"
 FT Domain 456..456
 FT /label= transmembrane domain
 FT /label= cytoplasmic domain
 FT /note= "GC and protein kinase activity"
 FT Modified-site 24..26
 FT /label= N-glycos_ site
 FT Modified-site 35..37
 FT /label= N-glycos_ site
 FT Modified-site 161..163
 FT /label= N-glycos_ site
 FT Modified-site 195..197
 FT /label= N-glycos_ site
 FT Modified-site 244..246
 FT /label= N-glycos_ site
 FT Modified-site 277..279

FT /label= N-glycos_ site
 FT Modified-site 349..351
 FT /label= N-glycos_ site
 FT Modified-site 600..602
 FT /label= N-glycos_ site

XX WO9100292-A.

XX 10-JAN-1991.

XX 22-JUN-1990; 90WO-0503586.

XX 23-JUN-1989; 89US-0370673.

XX (GENTH) GENENTECH INC.

XX Chang M, Goeddel D, Lowe D;

XX WPI; 1991-036711/05.

PT Natriuretic protein receptor B - for diagnosis and treatment of
 CC kidney failure, heart failure, hyperaldosteronism, glaucoma etc.

PS Claim 27; Disclosure: 49pp; English.

XX The sequence is that of a variant of natriuretic peptide receptor B
 CC (NPBR).

CC Editor's note: the AAs replaced in the sequence do not correspond
 CC to those of NPBR given in the specification (see p.27, 1.23-27;
 CC figs. 1 and 2), but instead to AAs in the sequence provided for
 CC NPBR (fig. 2). The origin of the AAs to be substituted is not
 CC clear; they may be taken from the sequence of rat NPBR (p.8, 1.18;
 CC p.9, 1.33) or rat NPBR (p.27, 1.20). The substitution indicated on
 CC p.9, 1.33, i.e. "phe644" is thought to be an error and should read
 CC "phe664".

CC The mutant was produced by modifying the DNA encoding the
 CC native sequence. The protein has guanyl cyclase (GC) activity and
 CC protein kinase activity. The DNA can be inserted into expression
 CC vectors for the prodn. of the NPBR analogue. The protein can be
 CC used in treatment of natriuretic peptide disorders, and also to
 CC isolate peptides using affinity chromatography. Antibodies with
 CC affinity for NPBR can also be prep'd.

CC See also AAR10399.

XX

XX Sequence 1047 AA;

Query Match 12.8%; Score 460; DB 12; Length 1047;
 Best Local Similarity 41.9%; Pred. No. 2.5e-34;
 Matches 113; Conservative 39; Mismatches 76; Indels 42; Gaps 6;

QY 411 DVTLIGEARAD-----GLKRLGK-----LKAATLEQA 439
 DB 760 ELVLLMERCWADPAERPDFOGIRFRFKEGSTILDMLLRMEQYANLEKIVEER 819
 QY 440 HQALEEKKKTVDLICSFPCVAAQOLMGQVQAKKSNVTMLFSDIVGFAISCQSP 499
 DB 820 TQATLEERKKAALYQILPHSVAEQLRGETVQAEADSVITFSYDVGFTALSAESTP 879
 QY 500 LQVITMLNALTFRDQCGELDYKVEITGDAYCAGGL-HKESDTHAVQIALMKME 558
 DB 880 MQVTLNLDLYTCEDAIIDNFDYKVEITGDAYVWSGLPGRNGORHAPETARALALL- 938
 QY 559 LSDEYMS-----PHGEPIKRIKIGHSVFAGVGVMPRYCLFGNNVTIANFESCSV 612
 DB 939 --DAVSSFRIRHPR-DQLRLRIGVHTGVCAGVGLKMPRYCLFGDVTNASHMESNGQ 995

QY 613 PRKINVSPTTYRLKDCGPFVTPRSREEL 642
 DB 996 AKTIHVSSTKDALDELGCFOLELRGDYEM 1025

RESULT 14

AAR38662

Wed Jul 2 12:21:11 2003

us-09-762-767a-2.rag

Page 12

Db 994 LFQDTVNTASRMSNGEALKIHLSEETKAVLEEEFGGFELELRGDVEM 1040

Search completed: June 27, 2003, 13:03:00
Job time : 39.3713 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2003, 13:03:07 ; Search time 19.5034 Seconds
(without alignments)
3401.080 Million cell updates/sec

Title: US-09-762-767a-2

Perfect score: 3593
Sequence: 1 MFCRLKDKITGECPSFL.....QKQVEDGNANFLKASGID 690

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3332	90.0	690	1 OYRTAI	guanylate cyclase
2	3171.5	88.3	717	2 S23098	guanylate cyclase
3	3107.5	86.5	691	1 OYBO77	guanylate cyclase
4	1635	45.5	732	2 S18325	guanylate cyclase
5	976.5	27.2	683	2 JH0810	guanylate cyclase
6	795	22.1	619	1 OYRTB1	guanylate cyclase
7	793.5	22.1	619	1 OYBO70	guanylate cyclase
8	789.5	22.0	619	1 S23097	guanylate cyclase
9	774.5	21.6	682	1 OYRTB2	guanylate cyclase
10	749.5	20.9	751	2 T24458	hypothetical prote
11	587	16.3	685	2 T19968	hypothetical prote
12	582.5	16.2	686	2 T23721	hypothetical prote
13	581	16.2	1099	2 T16822	hypothetical prote
14	551.5	15.3	699	2 T18984	hypothetical prote
15	493.5	13.7	583	2 F88642	protein C54E4.3 [1
16	463.5	12.9	1057	2 T15720	hypothetical prote
17	460	12.8	1047	1 OYHDB	natriuretic peptid
18	460	12.8	1047	1 OYRTB	atrial natriuretic
19	460	12.8	1047	1 I45882	atrial natriuretic
20	457.5	12.7	1057	1 OYRT	guanylyl cyclase A
21	457.5	12.7	1057	2 I55319	natriuretic peptid
22	456.5	12.7	1061	1 OYHDB	natriuretic peptid
23	454.5	12.6	1057	2 I57963	natriuretic peptid
24	452	12.6	1100	2 T42260	atrial natriuretic
25	449.5	12.5	1057	1 OYMSAR	atrial natriuretic
26	448	12.5	1108	2 A55915	guanylate cyclase
27	442	12.3	1108	2 J55385	guanylate cyclase
28	440	12.2	1103	2 J55581	guanylate cyclase
29	438	12.2	1108	2 B55915	guanylate cyclase

30	438	12.2	1110	1 S55279	guanylate cyclase
31	436	12.1	632	2 T31666	natriuretic peptid
32	435	12.1	1102	2 JH0717	guanylate cyclase
33	434	12.1	632	2 T31667	guanylate cyclase
34	430	12.0	1110	2 I59370	guanylate cyclase
35	428.5	11.9	1050	2 S45636	natriuretic peptid
36	428.5	11.9	1130	2 A89130	guanylate cyclase
37	428	11.9	1068	2 T42382	guanylate cyclase
38	427	11.9	1125	1 OYRCP	speract receptor p
39	423.5	11.8	1525	1 A56699	guanylate cyclase
40	420.5	11.7	1005	2 S33525	guanylate cyclase
41	418	11.6	1012	2 T24384	hypothetical prote
42	418	11.6	1170	2 T27564	hypothetical prote
43	414	11.5	1144	2 T21223	hypothetical prote
44	412.5	11.5	1122	2 T28130	hypothetical prote
45	411.5	11.5	540	2 T34187	hypothetical prote

ALIGNMENTS

RESULT 1

OYRTAI
guanylate cyclase (EC 4.6.1.2), soluble, alpha-1 chain - rat

N:Alternate names: guanylate cyclase, soluble, 77k chain
C:Species: Rattus norvegicus (Norway rat)

C>Date: 31-Mar-1993 #sequence_rev10 31-Mar-1993 #text_change 18-Jun-1999

C:Accession: A38297

R:Nakane, M.; Arai, K.; Saheti, S.; Kuno, T.; Buechler, W.; Murad, F.
J. Biol. Chem. 265, 16841-16845, 1990

A:Title: Molecular cloning and expression of cDNAs coding for soluble guanylate cyclase

A:Reference number: A38297; PMID:1009100; PMID:1698769

A:Accession: A38297

A:Molecule type: mRNA

A:Residues: 1-690 <NA>

A:Cross-references: GB:M57405; GB:M36075; NID:g204277; PIDN:AAA41206.1; PID:g204278

C:Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic domain homology

C:Keywords: GMP biosynthesis; heterodimer; phosphorus-oxygen lyase

F:432-660/Domain: guanylate cyclase catalytic domain homology <GCC>

Query Match	Score	DB 1	Length	690
Best Local Similarity	89.18	Pred. No. 4,6e-217		
Matches 616; Conservative 39; Mismatches 34; Indels 2; Gaps 2;				
OY	1	MFCRLKDKITGECPSFLAPGVNSESSEASGSCATVPICODIPKNIQESLP	60	
Db	1	MFCRLKDKITGECPSFLAPGVNSESSEASGSCATVPICODIPKNIQESLP	59	
OY	61	QRTSRVYVLTPLAESICKLIFPERLNVALQRTIAHKIKESKSLERDEFTIAE	120	
Db	60	QRTSRVYVLTPLAESICKLIFPERLNVALQRTIAHKIKESKSLERDEFTIAE	119	
OY	121	QAVAGVPEVVKESGEVEFKICVEDNIIIGVGGITKDLNLSSTLKSSHQEQNG	180	
Db	120	EALAGVPEVVKESGEVEFKICVEDNIIIGVGGITKDLNLSSTLKSSHQEQNG	179	
OY	181	KGRLEDAIILCDKEDDLAHYFFPKRTSILPGIITKAHAHYETEVEVSLMPCE	240	
Db	180	KGRLEDAIILCDKEDDLAHYFFPKRTSILPGIITKAHAHYETEVEVSLMPCE	239	
OY	241	HNDSEFVNOPIYLVSVHKSSTPSKPOSSIVPTSLFCKTFFHFMEDKMTIQ	300	
Db	240	HNDSEFVNOPIYLVSVHKSSTPSKPOSSIVPTSLFCKTFFHFMEDKMTIQ	299	
OY	301	PNGIRRLMNRDDEGKPEEVEFTLTKINOTSGITMNMQVAVVRWDNSYKKS	360	
Db	300	PNGIRRLMNRDDEGKPEEVEFTLTKINOTSGITMNMQVAVVRWDNSYKKS	359	
OY	361	SRVMDKGMIIYVESAILFLGSPVDLEDFGTGLYSDIPINALRDVYLIGEQR	420	
Db	360	SRVMDKGMIIYVESAILFLGSPVDLEDFGTGLYSDIPINALRDVYLIGEQR	419	
OY	421	AODGLKRLGKLKATLEQAHQALEEKKRTVDLLCSIFPCEVAQQLMOGVVQAKFSNV	480	


```

Db      421 RQDDILKRLGKLTLEAHQALEEKKRTVDLLCSIPSEVAARLQMGHVAQARFQ 480
QY      480 VTMLFSDIYGFALISQCSPLQVITMLNLYTRPDQCGELQYKVTIGDAYCVAGLH 539
Db      481 VTMLFSDIYGFALISQCSPLQVITMLNLYTRPDQCGELQYKVTIGDAYCVAGLH 540
QY      540 RESDTHAVQIALMALKMMELSDVMSPHGEPIKMRIGLHSGSVFAGVGVKMPRYCLFQ 599
Db      541 RESDTHAVQIALMALKMMELSDVMSPHGEPIKMRIGLHSGSVFAGVGVKMPRYCLFQ 600
QY      600 NTLANKEESCVCSPKINSPPTTYRLKCKPGVFYTPKRSRELPPRPSEIPIGICFLDA 659
Db      601 NTLANKEESCVCSPKINSPPTTYRLKCKPGVFYTPKRSRELPPRPSEIPIGICFLDA 660
QY      660 YQGTNSKRCFQKQKVDGDNANFLGKASGID 690
Db      661 YQGTNSKRCFQKQKVDGDNANFLGKASGID 691

```

RESULT 4

```

S18325
guanylate cyclase, soluble, alpha chain - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C:Accession: S18325
R:Harteneck, C.; Wedel, B.; Koesling, D.; Malkewitz, J.; Boehme, E.; Schultz, G.
FEBS Lett. 292, 217-222, 1991
A:Title: Molecular cloning and expression of a new alpha-subunit of soluble guanylyl cyclase.
A:Reference number: S18325; MUID:92070494; PMID:1683630
A:Accession: S18325
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-732 <HAR>
A:Cross-references: EMBL:X63282; NID:931670; PID:CAA44921.1; PID:931671
C:Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic domain homology
F:473-701/Domain: guanylate cyclase catalytic domain homology <GCC>

```

Query Match

```

Best Local Similarity 45.5%; Score 1635; DB 2; Length 732;
Matches 355; Conservative 106; Mismatches 200; Indels 58; Gaps 15;

```

```

QY      13 GECPSLA-----PGQPNSESEAAAGSESCATVPTCODIPKNIQESLPQRTS 65
Db      27 GECPSLRICWNGSRSPG---PLEPSPAAAAA---AAPATPAASAAAAAATAGARRVOR 81
QY      66 RSRVYLHTLAESICKLIPPEFRLNVALQRTLA--KHKT---KESKSL-----109
Db      82 RRRVNLDSIGESISRLTAPSPOTIOOTLKRITQYEHQYIGRDAKKNHINISNRCSTAD 141
QY      110 -----EREDFEKTIAEQAAVAGVPEVNIKESLGEVEFKICYEDENILGVGGTLDFLN 164
Db      142 HSNKEIEDVSGILCTANILGKFEIQRGEFFNICFHEHNEHVALVAVGGTLDFDN 201
QY      165 SFTILLKQSHQGA--GKRGRLDASILCLDKEDFLAHYFFPKRTTSLILPGITKAA 223
Db      202 GDDALLE---HRTSPGQATLESPEFLCKELPEGLIMLHYPHPIVGFAMIGMKAAG 258
QY      224 HVLTEVEVSLMPCFHNND--CSEFVNOP---YLLSYHMKSTKSLSPKPOSSLVP 278
Db      259 KRIYLDVVEQVA---NEKICSD--VSNPGKSCITFLIKCEKENTINIKNLPQGSQVP 313
QY      279 TSL-----FCKTFPHFEMFDKMTLLQFNGIRLMLNRDPOGKNPEFEYELPKIN 332
Db      314 ADLRISINIFCRAFPFLHMFDESMVYLQEGELRQD--RCDPHKVLKFEDECFEIVSPKN 372
QY      333 QFESGIMTLNMQVVRVRMRDMSYKSSRVMDIKOMTIYVSSAILLGLSCVRLD 392
Db      373 AFPERLRLSTPEVLRITPEASGSSENKQVMEVKQMHPESNIIELGSCVRLD 432
QY      393 FTGGRGLYSDIDIRHNLADVYLIGEQARAODGLKRLGKATLEQAHQALEEKKRTYD 452
Db      433 LMGRLHLSIDIRIHATRVYILVGEQAKADGLKRMKDKATLEHQALEEKKRTYD 492

```

```

QY      453 LLSIPCEVAQOLMGOVVOAKKFSNTMLSDIYGFALISQCSPLQVITMLNLYTR 512
Db      493 LLSIFPSGVAQOLMGOVVOAKKFSNTMLSDIYGFALISQCSPLQVITMLNLYTR 552
QY      513 FPOQCGELDYKVTIGDAYCVAGLHKSQSDTHAVQIALMALKMMELSDVMSPHGEPIK 572
Db      553 FPOQCGELDYKVTIGDAYCVAGLHKSQSDTHAVQIALMALKMMELSDVMSPHGEPIK 612
QY      573 MRIGHSGSVFAGVGVKMPRYCLFQNNNTLANKEESCVCSPKINSPPTTYRLKCKPGF 632
Db      613 MRIGHSGSVFAGVGVKMPRYCLFQNNNTLANKEESCVCSPKINSPPTTYRLKCKPGF 672
QY      633 VFTPRSRELPPRPSEIPIGICFLDAYOQGTNSKRCFQKQKVDGDNAN---FLGKAS 687
Db      673 VFTPRSRELPPRPSEIPIGICFLDAYOQGTNSKRCFQKQKVDGDNAN---FLGKAS 731

```

RESULT 5

```

JH0810
guanylate cyclase (EC 4.6.1.2) - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 26-Aug-1999
C:Accession: JH0810
R:Toshikawa, S.; Miyamoto, I.; Aruga, J.; Furutachi, T.; Okano, H.; Mikoshiba, K.
J. Neurochem. 60, 1570-1573, 1993
A:Title: Isolation of a Drosophila gene encoding a head-specific guanylyl cyclase.
A:Reference number: JH0810; MUID:93203896; PMID:8095978
A:Accession: JH0810
A:Molecule type: mRNA
A:Residues: 1-683 <YOS>
A:Cross-references: GB:S57126; NID:q298674; PID:q298675
A:Experimental source: head
C:Genetics:
A:Gene: dgc 1
A:Cross-references: FlyBase:Fgn0010227
C:Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic domain homology
C:Keywords: GMP biosynthesis; phosphorus-oxygen lyase
F:417-641/Domain: guanylate cyclase catalytic domain homology <GCC>

```

```

Query Match 27.2%; Score 976.5; DB 2; Length 683;
Best Local Similarity 37.3%; Pred. No. 5.1e-60;
Matches 244; Conservative 116; Mismatches 211; Indels 83; Gaps 20;

```

```

QY      58 SLPORTSRKRYLHTLAESICKLIPPEFRLNVALQRTLA-----HKIK---ESR 106
Db      27 ALDEDELSDALFTLHLQALQTLTAPSNEDLTATSLYAKRQWMPNHIKTLKDPQTF 86
QY      107 KSLERDEFTIAE-----QAVAGVPEVNIKESLGEVEFKICYEE--DENILGVVGT 159
Db      87 KSCANDYDLADIOELLKMDASASBILV-----LIGBELTCCCGIITERAFRCIGTDL 141
QY      160 KDFLNSFS---TLKQSHQGAEGKRGRLDASILCLDKEDFLAHYFFPKRTTSLILP 216
Db      142 QEFVSLDGVYDLK---LQED---YTDGFCVAGBEE---LTFSERVIMWLL 189
QY      217 GIITKAHLYETEVEVSLMPCFHNDCSEFVNOPYL---YSVHMKSTKSLSPKPO 272
Db      190 GSKALTRMLYKVDVNIKIEPV-----ERCVAVSLPILLAGGQGLPDHADSSTSVSTIPE 245
QY      273 -----SSLVITSLFCKTFPHFEMFDKMTLLQFNGIRLMLNRDPOGKNPEFE 322
Db      246 TVORSNSNNAISDLOMNSSSFCCKMFPWHFIMNBOLEIYOLGRFSKLY-----KPYMAD 298
QY      323 -----YFELTPK--INQFSGIMTLNMQVVRVRMRDMSYKSSRVMDIKOMTIY 374
Db      299 FGCQATTYEDFKPKKGLTKFRTYVTRITTYFLIGLNNPAGVDFPAIGLEIGQWHP 358
QY      375 ESSAILFLSPCYRLDEFTGRLYSDIDIRHNLADVYLIGEQARAODGLKRLGKAT 434
Db      359 ESNSTLIFGSPFLDGLDGLCNGLFTSIDIRHATREVLIVGQARAODGLRRRMDKIN 418
QY      435 TLEQAHQALEEKKRTYDVLCSIFPCEVAQOLMGOVVOAKKFSNTMLSDIYGFALIS 494

```



```

Db      491 HHASICHALDAMEIAGV-QVDSVOITIGITGEVYGVICQRPRLFGNVNL 549
OY      604 ANKESCSVPKRIINVSPTTYRLKDCPGFVTPRSREELPPNPFSEIPG 652
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      550 TSRTETGEKGINVSEYTRCL-----MTP---ENSDPQHLEHNG 588

RESULT 8
S33097
guanylate cyclase (EC 4.6.1.2), soluble, 70K chain - human
C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 20-Apr-2000
C:Accession: S23097
R:Gi111, G.; Scholl, U.; Buller, F.; Guellaen, G.
FEBS Lett. 304, 83-88, 1992
A:Title: Molecular cloning of the cDNAs coding for the two subunits of soluble guanylyl
A:Reference number: S23097; MUID:92316204; PMID:1352257
A:Accession: S23097
A:Molecule type: mRNA
A:Residues: 1-619 <GIT>
A:Cross-references: EMBL:X66533; NID:g31685; PIDN:CAA47144.1; PID:g31686
C:Genetics:
A:Gene: GDB:GDCY1B3; GUC1B3; GC-SB3
A:Cross-references: GDB:141992; OMIM:139397
A:Map position: 4q31.3-4q33
C:Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic domain homology
C:Keywords: heterodimer; phosphorus-oxygen lyase
F:373-607/Domain: guanylate cyclase catalytic domain homology <GCC>

Query Match      22.0%; Score 789.5; DB 1; Length 619;
Best Local Similarity 35.1%; Pred. No. 4,7e-47;
Matches 207; Conservative 96; Mismatches 219; Indels 67; Gaps 15;

OY      101 KIKESKSLEREDFEKTIAEQAVAGVY-----EVIKESIGEEVFKICYED-ENILG 153
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      30 QLEDEGQFLVRIYDSTYDVAASKVLMNAGEIL-QMGKMFVYVQSGSDYTLIR 88
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      154 VVGGLKQFLNSFTLLKQSSHCQAGKRGLEDASIIICLDE-DDELHYVFPKRTTS 212
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      89 VLGSVAREFLQNLDA-----HDHLATYVPGKAPSFCTDAEKKGILHYSSREGIQ 143
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      213 LILPQIKAAAHVLEYETEVEVSLM-----PCPHNCCSEVNPYLLYSVHMSTPS--- 265
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      144 DIVIGITVTAQOIGTEIDMKVIOQRNEECDHQ-----FLIEEKSEEDFY 192
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      266 -----LSPSKQSSLIYPTSLFCKTFPFHFMEDKMTILQFNGIRLNRDFOGKPYF 320
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      193 EDLDREENGQESRISPYT-FCKAFPHIIFEDRLVYQCGNATYRVLPQIQ-PGNCSL 250
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      321 EEPFILLPKINOTFSGITMLNMQFVYVRRVNDNSVKK-----SSRYMDLKGOM 370
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      251 LSVFSLVRPHIDISPHGISLHINTFYVSKSGELDVEKLECEDELGTETISCLRLKGM 310
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      371 IYIVSSALIFLFGSCVRLDEFTGRGLYLSIDIPILHNLADVLIGEORADGLKRRIG 430
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      311 IYLPADSDILFSCSVANLDDLTGRGLSDIPILHNLADVLIGEORADGLKRRIG 370
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      431 KLKATLEQAOHLEBEKKRTVDLCSIFPCVEVAQOLMOGOVQAOKKFSVNTMLFSDYGF 490
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      371 ILTDLQTLRLALEDEKKKTDTLVSYPVAVANELRRHRRPAPKARYDVTILLFSGYGF 430
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      491 TALCSQCS-----PLQVITMLNALYTRPDQCGELD---YKVEITGDAYCVAGGLHESD 543
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      431 NAFCSKHAHSGEAMKIVMLNDLYTRFPLTIDSRKNPFYKVEITGDKMTVSGLEPECI 490
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      544 THAVQIALMALKMLLDEVMSPHGEPIKMRIGLHSGSVFAGVGVKMPRYCLFGNNVTL 603
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      491 HHASICHALDAMEIAGV-QVDSVOITIGITGEVYGVICQRPRLFGNVNL 549
OY      604 ANKESCSVPKRIINVSPTTYRLKDCPGFVTPRSREELPPNPFSEIPG 652
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      550 TSRTETGEKGINVSEYTRCL-----MSPENDDPQHLEHNG 588

```

```

RESULT 9
OYRTB2
guanylate cyclase (EC 4.6.1.2), soluble, beta-2 chain - rat
N:Alternate names: guanylate cyclase, soluble, 76K chain
C:Species: Rattus norvegicus (Norway rat)
C>Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Jun-1999
C:Accession: A36228
R:Yuen, P.S.T.; Potter, L.R.; Garbers, D.L.
Biochemistry 29, 10872-10878, 1990
A:Title: A new form of guanylyl cyclase is preferentially expressed in rat kidney.
A:Reference number: A36228; MUID:91105012; PMID:1980215
A:Accession: A36228
A:Molecule type: mRNA
A:Residues: 1-682 <YUE>
A:Cross-references: GB:M57507; GB:J05308; NID:g204279; PIDN:AAA41207.1; PID:g204280
A:Experimental source: kidney
C:Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic domain homology
C:Keywords: cGMP biosynthesis; heterodimer; phosphorus-oxygen lyase
F:360-584/Domain: guanylate cyclase catalytic domain homology <GCC>

Query Match      21.6%; Score 774.5; DB 1; Length 682;
Best Local Similarity 32.6%; Pred. No. 5.9e-46;
Matches 190; Conservative 107; Mismatches 204; Indels 81; Gaps 10;

OY      129 VEVIKESIGEEVFKICYED-ENILGVVGTLLKDLNFSHTLLKQSSHCQAGKRGRLD 187
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1 MEAILKLFEEYFFKCKKNGYDRLRTLGNTLEFIENDAL-----HSYLLSYQEMNA 55
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      188 ASIIICLKDADDLHYIYFFPKRTTSLILPGITKAAAHVLEYETEVEVSLMPPCFHNDGSEF 247
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      56 PSFVRVEEGADGAMLLHYSDRGILHYGIIIEAVALKDFPDVAMSTL-----DMNEE 109
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      248 V-----NOPYLLSYVHKSTKP--SLSPKROSS----- 274
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      110 VERTGKKEHVAVLVQAKARQIRGAKASNPQSSQADQELQGLLMKRYNTLPYC 169
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      275 -----LVIPTSLCKTFPFHFMEDKMTILQF 302
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      170 PGEKSHSTAVRASVLEFGKPLNDTFQYPERLWVEEYFCDAFPHIYFDEALRYKQG 229
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      303 NQIRRLNRDQGRNPFEEYFELPKINOTFSGITMLNMQFVYVRRV-WDNSYKSS 361
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      230 VNIQKVPGLIQ--KFADEYFSIIHPQTFNISSICKFINSQFVLTKEKMPKRRKQ 288
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      362 RYMDLKGOMIYVESAILFLGSPCYRLDEFTGRGLYLSIDIPILHNLADVLIGEORARA 421
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      289 PMLKIRGOMIMHESLRMTFCSPNVRSLQELIESKMHSLDAPHDITDILLINQORLA 348
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      422 QDGLKRLGLKATLEAOHLEBEKKRTVDLCSIFPCVEVAQOLMOGOVQAOKKFSVNT 481
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      349 EMELSQLEKKKEELRVLSNHLAIEKKKETILLYALPVRVANOQLEKGRVAAAGEPETCT 408
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      482 MFSIDVGTALCSQCSPIQVITMLNALTNRDQCGELDYYKVEITGDAYCVAGGLHES 541
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      409 ILFSDVYFTNTCAACEPIQIVNMLNSMYSKDRILTSHVDYKVEITGDAYVVGVPVP 468
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      542 SDTHAVQIALMALKMLLDEVMSP-HGEPPIKMRIGLHSGSVFAGVGVKMPRYCLFGNN 600
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      469 VESHQVRANPFLGMRISAKVEYRNPTGPIQIRGVIHGPVLGAGVGVKMPRYCLFGT 528
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      601 VTLANKFESCSVPKRIINVSPTTYRLKDCPGFVTPRSREEL 642
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      529 VNTASRMESHGLPSKVHLSPTHRALKN-KGEIYVRGEIEY 569
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
T24458
hypothetical protein T04D3.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C:Accession: T24458
R:Kreishaw, J.

```

submitted to the EMBL Data Library, October 1996

A:Reference number: Z19893

A:Accession: T24458

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-751 <W11>

A:Cross-references: EMBL:Z81114; PIDN:CA803288.1; GSPDB:GN00019; CESP:T04D3.4

A:Experimental source: clone T04D3

C:Genetics:

A:Gene: CESP:T04D3.4

A:Map position: 1

A:Insertions: 1/3; 26/2; 95/3; 149/1; 213/3; 247/3; 291/3; 332/3; 369/2; 418/1; 462/3; 498/

C:Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic domain homology

Query Match

Best Local Similarity 31.5%; Pred. No. 3,76-44;

Matches 192; Conservative 125; Mismatches 239; Indels 53; Gaps 16;

20.9%; Score 749.5; DB 2; Length 751;

116 KTAEQAVAAVPEVKESEGEVEKICEED-ENILGVGGTLPKPLNSFTLKOSS 174

50 RLNSMANVIGIPLEETWEAYGGLIQTMTGMDLRMAPDLEGLDLSLHYFID 109

175 HCEAGKRGRLDPSILCKEDDFLHYVEFPKRTSLIPGIIKAAHLYETEYVS 234

110 H---VYKTKLRGSPFCVDVQADCTLHLHYSKRSGLPYKGVREYARRITDYEVMK 166

235 LMP-PCFHNDCSEFVNOPYLLYSV---HMKSTKPSLSPKPOSLVPTSL-----F 282

167 VOERKQEHDA--FVTE-HVFEVITQJENANSSTPKSISSKADSIDLSGIYEISSDF 223

283 CKRPPEFHEMDKMTILIQPNGIRLRANRDFOCKPFEYFELLTKINOTSGIWTML 342

224 SLAPFHYICDPDLFVHFENFKITPPNA-MROETVTLLELVHPEVPSYSIKYK 282

343 NMOFVAVRRKDSNVKRS---SRVMDLKGMIYIVESSAILFLGSPCVDRLEDTGRLGY 399

283 NSLFEVFLKGLGDIHNADEAKVLLKGMVFIIDEKRIYLYMGSVATVYRELIERNLH 342

400 LSDPIFNALRDVYLLGEQARADGKRLKGLKATLEQAHQALEBEKKKTVDLCSIFP 459

343 LSPMRIDGTRDVIYMLNOSMSQVELNRTLEETTKIKKMAQELIEIKQTDIDELCLMP 402

460 CEVAQOLMOGOVQAKKFSNVTMLFSDIVGFTALICSCSPLOYTMNALYTRDOCGE 519

403 ASVADSLRSKADAKFACTLETFDVIYFTNCACTPDVATLNDLYLRDRVGL 462

520 LDVYKETTIGDAYCVAGLHRESPTHAVOIALMALKMMELSDVMSF--HGEPIKRIGL 577

463 HDAYKVTETIGDAYVIYGVPERCENHAEVRLNISIGMLMESKLVLSPTIH-KPIKIRLGV 521

578 HSGSVFAGVGVAMPKRCLEGNNTVLANKESSCVPRKINVSPT-TYRLKDCPGFVTP 636

522 HGPVYVAGVYGIKPRYCLFGDTVNVANKMESNGIOCKIHVSEKGLNGKANSYFID 581

637 RSRE-----LPPNFPSEIPGIC-----HFLDAYOQGTNSKCFQK----- 673

582 KGTELENGKAMTTFYLERNDKSWELCSRPNSGEQITDGYME-LHDQSIYDEGGQOE 640

674 --DVEDGNA 680

641 NLTVENGNNS 649

RESULT 11

T19968

hypothetical protein C46E1.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T19968; T23092

R:Lennard, N.

submitted to the EMBL Data Library, November 1997

A:Reference number: Z19205

A:Accession: T19968

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-685 <W11>

A:Cross-references: EMBL:AL008867; PIDN:CA15512.1; GSPDB:GN00028; CESP:C46E1.2

A:Experimental source: clone C46E1

R:Lennard, N.

submitted to the EMBL Data Library, October 1997

A:Reference number: Z19673

A:Accession: T23092

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-685 <W12>

A:Cross-references: EMBL:Z99942; PIDN:CA17073.1; GSPDB:GN00028; CESP:C46E1.2

A:Experimental source: clone H13N06

C:Genetics:

A:Gene: CESP:C46E1.2

A:Map position: X

A:Insertions: 11/3; 36/2; 70/1; 133/2; 179/1; 202/3; 258/2; 298/2; 301/3; 325/2; 405/2;

C:Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic domain homology

Query Match

Best Local Similarity 16.3%; Score 587; DB 2; Length 685;

Matches 185; Conservative 114; Mismatches 254; Indels 106; Gaps 20;

107 KSLERDEFEKTIAEQV-----AAGVPEVKESEGE--EVFKICEED-- 148

34 KVLERAGFEAG-KENIINHYSDADPESLVDASVILKREQVWEYGCFLIQTWETG 92

149 -ENILGVGGTLPKPLNSFTLKOSSH--QEGKRGRLDPSILCKEDDFLHYVEF 206

93 WDLIRMSNGLGFLDNLDSLHYFDHVVYKANKLR---PFRCDNDPGTTLHYTF 148

207 PKRTSLILPGIIRKAAHLYETEYVSL---MPCEHNDCSEFVNOPYLLYSVHM--- 259

149 GRGLYIVYGVYREAKRFFKLDVSWITIGRQSRVQATGRIER-HVIFVKTLMND 207

260 KSTKPSLSPKPOSLVPTSL---PCKFPFHEMDKMTILQNGNGIRLRANR--RD 313

208 QSNDEALGTVAVHSHNNYKIRLTHMDISTFPHYHVVDDCKIVQV--RELNYNHPKD 264

314 F--QKRPFEYFELLTPKINOTFSGIMTMNQFVVRVNRD---NSVKSSRYMD- 365

265 LLSVGRP-LMRIFVYRPPQIPDPDSICNINAVFVLYQVTTTMEORANKRAAQITA 323

366 -----LKGMIYIVESSAILFLGSPCVDRLEDTGRLGYLDIP 404

324 SENLYEDNNGALALSGQHILKRGQMLMSSGGHIMYICSPYVTSIPELLQYGLRLAMP 363

405 IHNALRBYVLIQDARADGLKRLKATLEQAHQALEBEKKKTVDLCSIFPCVAYQ 464

384 IHDPTRDLILLNQRLSDVENMLQLEANNDELNMAKDLVEVGKTDALLREMLPSVAYQ 443

465 QLMQGVQVQAKKFSNVTMLFSDIVGFTALICSCSPLOYTMNALYTRFOCGEGLDYK 524

444 QLMQGLSVEAREKEATVMTDPTPOQIYPLCTPKADIVALLMELPKFPRLLIGIQAYK 503

525 VETIGDAYCVAGLHRESPTHAVOIALMALKMMELSDVMSF--HGEPIKRIGLHSGSV 583

504 VETVGDYSMSVGGIPDLVDHCEVICHIALGVMEARVCDPTNPLPHIRAGIHSGPV 563

584 AGVYGVAMPKRCLEGNNTVLANKESSCVPRKINVSPTTYRLKDCPGFVTPRSRE-- 641

564 AGVYGVAMPKRCLEGNNTVLANKESSCVPRKINVSPTTYRLKDCPGFVTPRSRE-- 641

642 -----LPPNFPSEIPGIC-----HFLDAYOQGTNSKCFQK----- 673

624 GKEMNTYPLLRFSFKSIWEIILRRDENCNSIDGYNELREGVYDVLYANKVTKNSKTC 682

RESULT 12

T23721

hypothetical protein M04G12.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

A:Residues: 1-699 <WIL>
 A:Cross-references: EMBL:Z77652; PIDN:CA801118.1; GSPDB:GN00023; CESP:C06B3.8
 A:Experimental source: clone C06B3
 C:Genetics:
 A:Gene: CESP:C06B3.8
 A:Map position: 5
 A:Insertions: 1/3; 60/1.192/3; 210/2; 270/2; 336/2; 415/2; 659/1
 C:Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic domain homology

Query Match 15.3%; Score 551.5; DB 2; Length 699;
 Best Local Similarity 26.6%; Pred. No. 2.1e-30;

Matches 153; Conservative 112; Mismatches 240; Indels 71; Gaps 12;

```

129 VEYKESLGEV--FKICEED--ENILGVGGLDPLNFSFTLLKQSH--COEAKR 182
      : : : : : : : : : : : : : : : : : : : : : : : : : :
59 LKVTQDVMEMVGGFLLTYSMEIGMDLVSMSPNLGFLDNLSDHYFDHYVYKMLR 118
      : : : : : : : : : : : : : : : : : : : : : : : : : :
183 GRLEDAIICLDKEDDLHYFFPKRTSLIPGIIIAAAHYETEVEVSLM---PPC 239
      : : : : : : : : : : : : : : : : : : : : : : : : : :
119 G---PSPCEEPDGTLLHYFTGRGLHYIVGVYAKRVEDIDITLVVGRTORS 174
      : : : : : : : : : : : : : : : : : : : : : : : : : :
240 FHNDCSEFVNO-----PYLXSVHKSTKPSLSPKPOSSLIPTSL---281
      : : : : : : : : : : : : : : : : : : : : : : : : : :
175 VHMNGRVEEHVVELINKGGOEHPPLI-AIVTGEPRRDSGSEVSLTSTNANPT 233
      : : : : : : : : : : : : : : : : : : : : : : : : : :
282 -----FCKTFPHFMDKMTILQFNGIRLNRNDQGRPNFEVEYFELLTP 329
      : : : : : : : : : : : : : : : : : : : : : : : : : :
234 IVDTLGISLDFSEKALPYHFVIDESCKLVCGSELNHNIPNELQGTPLIRIFEINRP 293
      : : : : : : : : : : : : : : : : : : : : : : : : : :
330 KINOTFGIMTMNMOFVVRV-----RWDNSVKRSSNVMD-----365
      : : : : : : : : : : : : : : : : : : : : : : : : : :
294 QIPLDFENIGNFINAVVLOVKTSP LKKHMDAMSQELKQEMTLEDATNELTQGHLL 353
      : : : : : : : : : : : : : : : : : : : : : : : : : :
366 -LKGOMIYVSSAILEFLGSPCYDRLEDTGRGLYSLDIPINALRDVVLIGEQAQDG 424
      : : : : : : : : : : : : : : : : : : : : : : : : : :
354 KLKGOMMLASKRIIITLSPYVTSINELMQYGRMLAMP LHDATRLILLNQRLSDVE 413
      : : : : : : : : : : : : : : : : : : : : : : : : : :
425 LKRLGLKATLRBAHALBEKKIYDILCSIFPCEVAQQLMGOVYQAKKSNVMTLF 484
      : : : : : : : : : : : : : : : : : : : : : : : : : :
414 VNLQLEANNQLEMTLELERKQTSILKDMIPRIAOQLSGEHIACE-HEAVYMF 472
      : : : : : : : : : : : : : : : : : : : : : : : : : :
485 SDIYGFALISCSPLQVITNLTALYTRFOCGELVYKVEITGDAYCVAAGLHKESDT 544
      : : : : : : : : : : : : : : : : : : : : : : : : : :
473 CDLPAPQOALPQCSKRIYVMMNIEFRKDRIVIRGVYKVEYSDSYMAVSGIPDTPE 532
      : : : : : : : : : : : : : : : : : : : : : : : : : :
545 HAVOIALMALKMLSDVMSPHGE-PIKMRIGLSGSVFAVGVYKMPRYCLFGNNVTL 603
      : : : : : : : : : : : : : : : : : : : : : : : : : :
533 HAENMCHVALGMMWEARSVIDPVSKTPFLRIGHSCTITAGVGVTHPRKCLFGEVTL 592
      : : : : : : : : : : : : : : : : : : : : : : : : : :
604 ANKFESGVPKRTIVSPFTRRLKDCPGFVTPRSR 639
      : : : : : : : : : : : : : : : : : : : : : : : : : :
593 ASQMESLGMAGKIQCKSMAYQAKMETGRFEFSPGR 628
      : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 15

F88642

Protein C54E4.3 [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001

C:Accession: F88642

R:anonymous, The C. elegans Sequencing Consortium.

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog

A:Reference number: A75000; MUID:99069613; PMID:9851916

A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C.ela

A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A:Accession: F88642

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-583 <STO>

A:Cross-references: GB:chr_IV; PIDN:AAB92031.1; PID:g2702405; GSPDB:GN00022; CESP:C54E4.

C:Genetics: Similar to guanylate cyclase

A:Gene: C54E4.3
 A:Map position: 4

Query Match 13.7%; Score 493.5; DB 2; Length 583;

Best Local Similarity 25.7%; Pred. No. 1.8e-26;

Matches 139; Conservative 129; Mismatches 218; Indels 55; Gaps 13;

```

122 AVAAGVVEVYKESIGE-EYFKICEEDENILGVGGLDPLNFSFTLLKQSHCOEAG 180
      : : : : : : : : : : : : : : : : : : : : : : : : : :
50 ATYVGLSDVDMEMVGGFLLTHACETGWMQMLPOMANNLODFLNLNSM---HYFDQIA 106
      : : : : : : : : : : : : : : : : : : : : : : : : : :
181 KRGLEDAIICLDKEDDLHYFFPKRTSLIPGIIIAAAHYETEVEVSLMPPCF 240
      : : : : : : : : : : : : : : : : : : : : : : : : : :
107 FKSEMKPTPOCEPFGSGGLKHYFSRQGLFPIYKGLVKTARTLPEMDVYKMLERNQ 166
      : : : : : : : : : : : : : : : : : : : : : : : : : :
241 HNDCEEVNQPYLXSVH-----MKST-----PSLSKPOSSLIPTSL 281
      : : : : : : : : : : : : : : : : : : : : : : : : : :
167 ERKSGMVE--HYFSVEPDNNHKKGRRLPHKRNITTNADSEFTLS---STLVGLRD 221
      : : : : : : : : : : : : : : : : : : : : : : : : : :
282 FCKTFPHFMDKMTILQFNGIR--LMNRDFOGRPNFEVEYFELLTPK-INOTFGS 337
      : : : : : : : : : : : : : : : : : : : : : : : : : :
222 FKNIFPVHVCENQMIEHIGIYLLREYGLENKTKL---VSDLMQLVQPSDIQLYKN 277
      : : : : : : : : : : : : : : : : : : : : : : : : : :
338 IATMLNQFYVRRRMD--NSYKKS-----RYMDLKGOMIYVSSAILEFLGSPCYDRL 390
      : : : : : : : : : : : : : : : : : : : : : : : : : :
278 VLSYLTNLTFTFOLKHSKRNEVOGSESEAPQOPLVYKGEKMPINDGNSIIFICSPTHYV 337
      : : : : : : : : : : : : : : : : : : : : : : : : : :
391 EDFTGRGLYSLDIPINHALRDVVLIGEQAQDGLKRLGLKATLEBAHALBEKKKT 450
      : : : : : : : : : : : : : : : : : : : : : : : : : :
338 RDLNLKLYISDMPHMATDLYVNLNSRLICQHELNKKELETKKKKKMTEELVYKSOR 397
      : : : : : : : : : : : : : : : : : : : : : : : : : :
451 VDLCSIFPCEVAQQLMGOVYQA-----KKSNTVMTLSDIVGFTAISQSCP 499
      : : : : : : : : : : : : : : : : : : : : : : : : : :
398 DRLLFEVPPVIAELRAATVPALMQRISIDFSEFSQCSYFTDIPDFTISVNCSP 457
      : : : : : : : : : : : : : : : : : : : : : : : : : :
500 LQVITMNLATYTRFOCGELDYKVTETIDACVAGGLKESDTNAVOIALMALKML 559
      : : : : : : : : : : : : : : : : : : : : : : : : : :
458 TEITVTVDLPHRRDRIRERHKGKVLSDVSLVGVGNANQYHCEDSLIALGLLFE 517
      : : : : : : : : : : : : : : : : : : : : : : : : : :
560 SDEYMSPHGE-PIKMRIGLSGSVFAVGVYKMPRYCLFGNNVTLANKFESGVPKRTIV 618
      : : : : : : : : : : : : : : : : : : : : : : : : : :
518 AKQVYVPRKRSVRLRIGVAGCPVAGIVSQAPRPFVGLNTVNTVTSICSHSPGRVLY 577
      : : : : : : : : : : : : : : : : : : : : : : : : : :
619 S 619
      : : : : : : : : : : : : : : : : : : : : : : : : : :
578 S 578
      : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Search completed: June 27, 2003, 13:05:23
 Job time : 21.5034 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 27, 2003, 13:00:58 ; Search time 34.7899 Seconds
(without alignments)
4086.601 Million cell updates/sec

Title: US-09-762-767a-2

Perfect score: 3593
Sequence: 1 MFTKRLDKLKTGECFSLT.....OKKVEDGNANFLGRASGID 690

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Lasting first 45 summaries

- 1: SP_ARCHAEA:*
- 2: SP_BACTERIA:*
- 3: SP_FUNGI:*
- 4: SP_HUMAN:*
- 5: SP_INVERTEBRATE:*
- 6: SP_MAMMAL:*
- 7: SP_MNC:*
- 8: SP_ORGANELLE:*
- 9: SP_PHAGE:*
- 10: SP_PLANT:*
- 11: SP_PROTOZOA:*
- 12: SP_VIRUS:*
- 13: SP_VERTEBRATE:*
- 14: SP_UNCLASSIFIED:*
- 15: SP_VIRUS:*
- 16: SP_BACTERIAP:*
- 17: SP_ARCHAEA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3587	99.8	690	4	08TAH3
2	3266.5	90.9	691	11	09DBQ3
3	3265.5	90.9	691	11	09ERB3
4	2954	82.2	564	4	09NNW8
5	2014.5	55.9	678	13	09PW12
6	2009.5	55.8	678	13	P79997
7	2005	55.8	675	13	090VY5
8	1097	30.5	699	5	077105
9	991.5	27.6	676	5	024085
10	983.5	27.4	676	5	024085
11	823	22.9	620	11	08R5L4
12	788	21.9	617	13	090VY5
13	785.5	21.9	600	5	077106
14	784.5	21.8	742	11	091XJ7
15	781.5	21.8	620	11	054865
16	781	21.7	614	13	P79998

17	771.5	21.5	636	11	0920Q1	0920Q1 rattus norv
18	750.5	20.9	604	5	095NK5	095NK5 hemiceurot
19	749.5	20.9	751	5	002298	002298 caenorhabd
20	743	20.7	758	5	024086	024086 drosophila
21	743	20.7	787	5	09VA09	09VA09 drosophila
22	720.5	20.1	649	5	017010	017010 anopheles
23	661	18.4	940	5	076340	076340 manduca sex
24	642.5	17.9	690	5	09VFC5	09VFC5 drosophila
25	587	16.3	685	5	09XTE0	09XTE0 caenorhabd
26	582.5	16.2	686	5	P92006	P92006 caenorhabd
27	555	15.4	752	5	022301	022301 caenorhabd
28	551.5	15.4	699	5	017707	017707 caenorhabd
29	547	15.2	684	5	09B180	09B180 caenorhabd
30	493.5	13.7	583	5	044468	044468 caenorhabd
31	479	13.3	1047	13	09PW10	09PW10 xenopus lae
32	478	13.3	1276	5	08T8L6	08T8L6 caenorhabd
33	477	13.3	1055	13	09YGM3	09YGM3 oryzias lat
34	473	13.2	1055	13	09B0T1	09B0T1 oryzias lat
35	463.5	12.9	1057	5	018331	018331 caenorhabd
36	462	12.9	1076	5	09W2P1	09W2P1 drosophila
37	461	12.8	1112	5	09GR36	09GR36 heterodera
38	460	12.8	344	11	08R1P8	08R1P8 mus musculu
39	460	12.8	618	4	08TA93	08TA93 homo sapien
40	456.5	12.7	1172	5	09V079	09V079 drosophila
41	455.5	12.7	1056	13	09Y117	09Y117 squalus aca
42	454.5	12.6	1057	11	091X04	091X04 mus musculu
43	453.5	12.6	210	13	09NH71	09NH71 epratretus
44	453	12.6	1076	5	09VP19	09VP19 drosophila
45	452	12.6	1100	11	054884	054884 rattus norv

ALIGNMENTS

RESULT 1

AC 08TAH3 PRELIMINARY; PRT; 690 AA.
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Similar to guanylate cyclase 1, soluble, alpha 3.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC028384; AAH28384.1; -; D9B98FC04DB927 CRC64;
SQ SEQUENCE 690 AA; 77470 MW; D9B98FC04DB927 CRC64;

Query Match 99.8%; Score 3587; DB 4; Length 690;
Best Local Similarity 99.7%; Pred. No. 1.6e-272;
Matches 688; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY	1	MFTKRLDKLKTGECFSLAPQVNESSEKATVPICODIPEKNIDSLP	60
DB	1	MFTKRLDKLKTGECFSLAPQVNESSEKATVPICODIPEKNIDSLP	60
QY	61	ORKTSRYVLTSLAESTICKLIPPEERLVALQRTIAKHIRESKRSEREDFEKTIE	120
DB	61	ORKTSRYVLTSLAESTICKLIPPEERLVALQRTIAKHIRESKRSEREDFEKTIE	120
QY	121	QAAVAGVPEVVKESIGEVEFKICYEDENILGVGGLTKDPLNSETLKKSSHQEAG	180
DB	121	QAAVAGVPEVVKESIGEVEFKICYEDENILGVGGLTKDPLNSETLKKSSHQEAG	180
QY	181	KRRRLDASTLCDDKDDPLHYVFFPKRTSLILGIIKAAHVLVETEVSLMPPC	240
DB	181	KRRRLDASTLCDDKDDPLHYVFFPKRTSLILGIIKAAHVLVETEVSLMPPC	240

```

QY 241 HNDSEFVNOPYLLYSVHMKSTKPSLSPKSSSVIPTSFCCKTPEPFHFMEDKMTILQ 300
DB 241 HNDSEFVNOPYLLYSVHMKSTKPSLSPKSSSVIPTSFCCKTPEPFHFMEDKMTILQ 300
QY 301 FGNGIRRLNRRDFOCKPNEEFELLTPKINOTFGIMTLMNQVAVVRMDNSVYKS 360
DB 301 FGNGIRRLNRRDFOCKPNEEFELLTPKINOTFGIMTLMNQVAVVRMDNSVYKS 360
QY 361 SRVMDLKGOMIYVESATILFSGPCVDRLDEFTGRLGLSDIPINHALRDVYLGEQAR 420
DB 361 SRVMDLKGOMIYVESATILFSGPCVDRLDEFTGRLGLSDIPINHALRDVYLGEQAR 420
QY 421 AODGLKRRGLKATLEQAHQALEEKKKTVDLLCSIFPCVAAQOLMGOVVOAKKFSNV 480
DB 421 AODGLKRRGLKATLEQAHQALEEKKKTVDLLCSIFPCVAAQOLMGOVVOAKKFSNV 480
QY 481 TMLFSIYVFTALSCSPLOYITMNLALYTRPDQCGELDYKVTETIGDAYCVAGGLK 540
DB 481 TMLFSIYVFTALSCSPLOYITMNLALYTRPDQCGELDYKVTETIGDAYCVAGGLK 540
QY 541 ESDTHAVQIALMALKMMELSDVMSPHGEPKIKRIGLHSGSVAGVGVKMPRYCLFGNN 600
DB 541 ESDTHAVQIALMALKMMELSDVMSPHGEPKIKRIGLHSGSVAGVGVKMPRYCLFGNN 600
QY 601 VTLANKFESCVPRKINVSPTTYRLKDCPGFVTPRSRELPNPFSEIPGICHFIDAY 660
DB 601 VTLANKFESCVPRKINVSPTTYRLKDCPGFVTPRSRELPNPFSEIPGICHFIDAY 660
QY 661 OOGTNSKPCFOKRDVEDGNANFLGKASGID 690
DB 661 OOGTNSKPCFOKRDVEDGNANFLGKASGID 690

RESULT 2
Q9DBQ3 PRELIMINARY: PRT: 691 AA.
ID 09DBQ3:
AC 09DBQ3:
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE 1200016007RLK protein.
GN GUCY1A3 OR 1200016007RLK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=LUNG;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawaji J., Shihagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana H.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
RA Kuehl P., Lewis S., Matsuo T., Nikaido I., Pesole G., Quackenbush J.,
RA Schmitt L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RT Functional annotation of a full-length mouse cDNA collection.*
RL Nature 409:685-690(2001).
DR EMBL: AK004815; BAB23586.1;
DR HSP: P19687; IAWN.

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DR MGD: MGI:1926562; Gucy1a3.
DR InterPro: IPR001054; G_cyclase.
DR Pfam: PF00211; guanylate_cyc; 1.
DR SMART: SM00044; CYC1.
DR PROSITE: PS00452; GUANYLATE_CYCLASES_1; 1.
DR PROSITE: PS01253; GUANYLATE_CYCLASES_2; 1.
KW Lyase.
SQ
Sequence 691 AA; 77587 MW; FF8DDDC3CB0BBD7F CRC64;

Query Match
Best Local Similarity 89.7%; Pred. No. 2,1e-247;
Matches 620; Conservative 36; Mismatches 34; Indels 1; Gaps 1;

QY 1 MECTRLKDKLITTECPFSILAPGOVNPSSSEAGSSSEKATVPICODIPENKIQBSLP 60
DB 1 MECTRLKDKLITTECPFSILAPGOVNPSSSEAGSSSEKATVPICODIPENKIQBSLP 60
QY 61 ORKTSRSVYLHTLAESICKLIPFEFELNANALORTLAKHRTKRSLSREDEKTIAT 120
DB 61 ORKTSRSVYLHTLAESICKLIPFEFELNANALORTLAKHRTKRSLSREDEKTIAT 120
QY 121 QAVAGVPEVYIKESIEEVEFKICEEDENILGVVGTLDKDFLNSFSTLTKQSSHCQAG 180
DB 121 QAVAGVPEVYIKESIEEVEFKICEEDENILGVVGTLDKDFLNSFSTLTKQSSHCQAG 180
QY 181 KRGRLSDASITCLKEDDFLHVYFFPKRTTSLIPGIIKAAHVLYETEVEVSLMPCCF 240
DB 181 KRGRLSDASITCLKEDDFLHVYFFPKRTTSLIPGIIKAAHVLYETEVEVSLMPCCF 240
QY 241 HNDSEFVNOPYLLYSVHMKSTKPSLSPKSSSVIPTSFCCKTPEPFHFMEDKMTILQ 300
DB 241 HNDSEFVNOPYLLYSVHMKSTKPSLSPKSSSVIPTSFCCKTPEPFHFMEDKMTILQ 300
QY 301 FGNGIRRLNRRDFOCKPNEEFELLTPKINOTFGIMTLMNQVAVVRMDNSVYKS 360
DB 301 FGNGIRRLNRRDFOCKPNEEFELLTPKINOTFGIMTLMNQVAVVRMDNSVYKS 360
QY 361 SRVMDLKGOMIYVESATILFSGPCVDRLDEFTGRLGLSDIPINHALRDVYLGEQAR 420
DB 361 SRVMDLKGOMIYVESATILFSGPCVDRLDEFTGRLGLSDIPINHALRDVYLGEQAR 420
QY 421 AODGLKRRGLKATLEQAHQALEEKKKTVDLLCSIFPCVAAQOLMGOVVOAKKFSNV 480
DB 421 AODGLKRRGLKATLEQAHQALEEKKKTVDLLCSIFPCVAAQOLMGOVVOAKKFSNV 480
QY 481 TMLFSIYVFTALSCSPLOYITMNLALYTRPDQCGELDYKVTETIGDAYCVAGGLK 540
DB 481 TMLFSIYVFTALSCSPLOYITMNLALYTRPDQCGELDYKVTETIGDAYCVAGGLK 540
QY 541 ESDTHAVQIALMALKMMELSDVMSPHGEPKIKRIGLHSGSVAGVGVKMPRYCLFGNN 600
DB 541 ESDTHAVQIALMALKMMELSDVMSPHGEPKIKRIGLHSGSVAGVGVKMPRYCLFGNN 600
QY 601 VTLANKFESCVPRKINVSPTTYRLKDCPGFVTPRSRELPNPFSEIPGICHFIDAY 660
DB 601 VTLANKFESCVPRKINVSPTTYRLKDCPGFVTPRSRELPNPFSEIPGICHFIDAY 660
QY 661 OOGTNSKPCFOKRDVEDGNANFLGKASGID 690
DB 661 HHOGPSNKPFOQDVEDGNANFLGKASGID 691

RESULT 3
Q9ERL9 PRELIMINARY: PRT: 691 AA.
ID Q9ERL9:
AC Q9ERL9:
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE Soluble guanylyl cyclase alpha 1 subunit.
GN GUCY1A3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BAIB/C;
 RX MEDLINE=20461464; PubMed=10984516;
 RA Sharina I.G., Krumenacker J.S., Martin E., Murad F.;
 RT "Genomic organization of alpha 1 and beta 1 subunits of the mammalian
 RT soluble guanylyl cyclase genes";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:10878-10883(2000).
 DR EMBL: AF297082; AAG17446.1;
 DR HSSP: P19687; IANV.
 DR MGD: MGI:1926562; GuoY1a3.
 DR InterPro: IPR001054; G_cyclase.
 DR Pfam: PF00211; guanylate_cyc; 1.
 DR SMART: SM00044; CYC; 1.
 DR PROSITE: PS00452; GUANYLATE_CYCLASES_1; 1.
 DR PROSITE: PS0125; GUANYLATE_CYCLASES_2; 1.
 KM Lyase.
 SQ SEQUENCE 691 AA; 77573 MW; F9F40C3CB0BD7F CRC64;

Query Match 90.9%; Score 3265.5; DB 11; Length 691;
 Best Local Similarity 89.6%; Pred. No. 2.5e-247;
 Matches 619; Conservative 37; Mismatches 34; Indels 1; Gaps 1;

OY 1 MCTRLNDKITGECFSLAPGVNPSSEBAAGSSSEKATVPICODIPKNIQESTIP 60
 DB 1 MCTRLNDKITGECFSLAPGVNPSSEBAAGSSSEKATVPICODIPKNIQESTIP 60
 OY 61 MECKRFKDLKITGECFSLAPGVNPSSEBAAGSSSEKATVPICODIPKNIQESTIP 60
 DB 61 MECKRFKDLKITGECFSLAPGVNPSSEBAAGSSSEKATVPICODIPKNIQESTIP 60
 OY 61 ORKTSRNVYIHTLAESTICKLIPFEERLNVALORTLAKHKIKESKLERDEKTLAE 120
 DB 61 ORKTSRNVYIHTLAESTICKLIPFEERLNVALORTLAKHKIKESKLERDEKTLAE 120
 OY 121 QAVAGVVEVEIKESLGEVEFKICEEDENILGVVGGLTKDPLNFSSTLLKSSHCQEA 180
 DB 121 QAVAGVVEVEIKESLGEVEFKICEEDENILGVVGGLTKDPLNFSSTLLKSSHCQEA 180
 OY 121 EAIAGAVVEALKOSLGEVEFKICEEDENILGVVGGLTKDPLNFSSTLLKSSHCQEA 180
 DB 121 EAIAGAVVEALKOSLGEVEFKICEEDENILGVVGGLTKDPLNFSSTLLKSSHCQEA 180
 OY 181 KRGLEDASILCKDEDFLHYVFFPKRTSLIPGIKAAAHVLYTEVEVSIMPCF 240
 DB 181 KRGLEDASILCKDEDFLHYVFFPKRTSLIPGIKAAAHVLYTEVEVSIMPCF 240
 OY 181 RGRLEDASILCKDEDFLHYVFFPKRTSLIPGIKAAAHVLYTEVEVSIMPCF 240
 DB 181 RGRLEDASILCKDEDFLHYVFFPKRTSLIPGIKAAAHVLYTEVEVSIMPCF 240
 OY 241 HNDSEFNOPYLLAYVHMKSTKPSLSPKPOSSIVITPSLCKFPFHMDKMTLITQ 300
 DB 241 HNDSEFNOPYLLAYVHMKSTKPSLSPKPOSSIVITPSLCKFPFHMDKMTLITQ 300
 OY 241 RSDCEFNOPYLLAYVHMKSTKPSLSPKPOSSIVITPSLCKFPFHMDKMTLITQ 300
 DB 241 RSDCEFNOPYLLAYVHMKSTKPSLSPKPOSSIVITPSLCKFPFHMDKMTLITQ 300
 OY 301 FGNGIRLRANRDFOGKPNFEFEILPKINQFSGIMTMNMOFVVRVRRMDSVKS 360
 DB 301 FGNGIRLRANRDFOGKPNFEFEILPKINQFSGIMTMNMOFVVRVRRMDSVKS 360
 OY 301 LGNGIRLRANRDFOGKPNFEFEILPKINQFSGIMTMNMOFVVRVRRMDSVKS 360
 DB 301 LGNGIRLRANRDFOGKPNFEFEILPKINQFSGIMTMNMOFVVRVRRMDSVKS 360
 OY 361 SRVMDLKQOMIYVSSAILFLGSPCVRLDEDFTRGLYLSDIPIHNLRDVYLIGEQA 420
 DB 361 SRVMDLKQOMIYVSSAILFLGSPCVRLDEDFTRGLYLSDIPIHNLRDVYLIGEQA 420
 OY 361 SRVMDLKQOMIYVSSAILFLGSPCVRLDEDFTRGLYLSDIPIHNLRDVYLIGEQA 420
 DB 361 SRVMDLKQOMIYVSSAILFLGSPCVRLDEDFTRGLYLSDIPIHNLRDVYLIGEQA 420
 OY 421 AODGKRLKGLKATLEAHOALBEKKRYDILCSIPCEVAOOLMOGOVQAQKFSV 480
 DB 421 AODGKRLKGLKATLEAHOALBEKKRYDILCSIPCEVAOOLMOGOVQAQKFSV 480
 OY 421 AODGKRLKGLKATLEAHOALBEKKRYDILCSIPCEVAOOLMOGOVQAQKFSV 480
 DB 421 AODGKRLKGLKATLEAHOALBEKKRYDILCSIPCEVAOOLMOGOVQAQKFSV 480
 OY 481 TMLFSDIYGFTALCSQSPLOYITMLNLYTRFDQCGELDYKKEITIGDAYCVAGGLK 540
 DB 481 TMLFSDIYGFTALCSQSPLOYITMLNLYTRFDQCGELDYKKEITIGDAYCVAGGLK 540
 OY 481 TMLFSDIYGFTALCSQSPLOYITMLNLYTRFDQCGELDYKKEITIGDAYCVAGGLK 540
 DB 481 TMLFSDIYGFTALCSQSPLOYITMLNLYTRFDQCGELDYKKEITIGDAYCVAGGLK 540
 OY 541 ESDTHAVOIALMALKMELSDVMSPHGEPIKMRIGLHSGSVFAGVGVKMPRYCLFGNN 600
 DB 541 ESDTHAVOIALMALKMELSDVMSPHGEPIKMRIGLHSGSVFAGVGVKMPRYCLFGNN 600
 OY 541 ESDTHAVOIALMALKMELSDVMSPHGEPIKMRIGLHSGSVFAGVGVKMPRYCLFGNN 600
 DB 541 ESDTHAVOIALMALKMELSDVMSPHGEPIKMRIGLHSGSVFAGVGVKMPRYCLFGNN 600
 OY 601 VTLANKFESSCVPKRIINSPITRYLKLDCPGVFPFRSREELPPNPSPSPICHTFLAY 660
 DB 601 VTLANKFESSCVPKRIINSPITRYLKLDCPGVFPFRSREELPPNPSPSPICHTFLAY 660
 OY 661 -QGTNSKPCFOKDVDEGNANFLKASGID 690
 DB 661 HHGPNKSPFQDKVDEGNANFLKASGVD 691

RESULT 4
 O9NNW8 PRELIMINARY; PRT; 564 AA.
 AC O9NNW8
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Soluble guanylate cyclase large subunit (Fragment).
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE OF 1-0 FROM N.A.
 RX MEDLINE=20183694; PubMed=10717483;
 RA Zhou Y.H., Zheng J.B., Gu X., Li W.H., Saunders G.F.;
 RT "A novel Pax-6 binding site in rodent B1 repetitive elements:
 RT coevolution between developmental regulation and repeated elements";
 RL Gene 245:319-328(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Zhou Y.H.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF233750; AAF64043.1;
 DR EMBL: AF233746; AAF64043.1; JOINED.
 DR EMBL: AF233747; AAF64043.1; JOINED.
 DR EMBL: AF233748; AAF64043.1; JOINED.
 DR EMBL: AF233749; AAF64043.1; JOINED.
 DR HSSP: P19687; IANV.
 DR InterPro: IPR001054; G_cyclase.
 DR Pfam: PF00211; guanylate_cyc; 1.
 DR SMART: SM00044; CYC; 1.
 DR PROSITE: PS00452; GUANYLATE_CYCLASES_1; 1.
 DR PROSITE: PS0125; GUANYLATE_CYCLASES_2; 1.
 KM Lyase.
 FT NON-TER
 SQ SEQUENCE 564 AA; 63406 MW; 7056E249A7F98D5 CRC64;

Query Match 82.2%; Score 2954; DB 4; Length 564;
 Best Local Similarity 100.0%; Pred. No. 4.9e-223;
 Matches 564; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 127 VPEVEIKESLGEVEFKICEEDENILGVVGGLTKDPLNFSSTLLKSSHCQEA 186
 DB 1 VPEVEIKESLGEVEFKICEEDENILGVVGGLTKDPLNFSSTLLKSSHCQEA 186
 OY 187 DASILCKDEDFLHYVFFPKRTSLIPGIKAAAHVLYTEVEVSIMPCFHNDCSE 246
 DB 187 DASILCKDEDFLHYVFFPKRTSLIPGIKAAAHVLYTEVEVSIMPCFHNDCSE 246
 OY 247 FVNOPYLLAYVHMKSTKPSLSPKPOSSIVITPSLCKFPFHMDKMTLITQNGIR 306
 DB 247 FVNOPYLLAYVHMKSTKPSLSPKPOSSIVITPSLCKFPFHMDKMTLITQNGIR 306
 OY 307 RLNRNDRDFOGKPNFEFEILPKINQFSGIMTMNMOFVVRVRRMDSVKSRYMDL 366
 DB 307 RLNRNDRDFOGKPNFEFEILPKINQFSGIMTMNMOFVVRVRRMDSVKSRYMDL 366
 OY 367 KQOMIYVSSAILFLGSPCVRLDEDFTRGLYLSDIPIHNLRDVYLIGEQAQDGLK 426
 DB 367 KQOMIYVSSAILFLGSPCVRLDEDFTRGLYLSDIPIHNLRDVYLIGEQAQDGLK 426
 OY 427 KRLGKRLKATLEAHOALBEKKRYDILCSIPCEVAOOLMOGOVQAQKFSV 486
 DB 427 KRLGKRLKATLEAHOALBEKKRYDILCSIPCEVAOOLMOGOVQAQKFSV 486
 OY 487 IYGFALCSQSPLOYITMLNLYTRFDQCGELDYKKEITIGDAYCVAGGLHKSSTHA 546
 DB 487 IYGFALCSQSPLOYITMLNLYTRFDQCGELDYKKEITIGDAYCVAGGLHKSSTHA 546
 OY 547 VOIALMALKMELSDVMSPHGEPIKMRIGLHSGSVFAGVGVKMPRYCLFGNNVTLANK 606
 DB 547 VOIALMALKMELSDVMSPHGEPIKMRIGLHSGSVFAGVGVKMPRYCLFGNNVTLANK 606

Db	421	VOJALNALKMMELSDVEMSPHEPIKMRIGLHSGSVFVGVKKPBCRLGNNVTLANK	480
Qy	607	FEGCSVPKRIKNSPTTYRLLKDCPGFVFPKRSRELPPNFSELPICHELDAVOQSTNS	666
Db	481	FEGCSVPKRIKNSPTTYRLLKDCPGFVFPKRSRELPPNFSELPICHELDAVOQSTNS	540
Qy	667	KPCFORKDVEDGNANFLKSGASGD	690
Db	541	KPCFORKDVEDGNANFLKSGASGD	564
RESULT 5			
ID	Q9PM12	PRELIMINARY;	PRT; 678 AA.
AC	Q9PM12;		
DT	01-MAY-2000 (Tremblrel. 13, Created)		
DT	01-MAY-2000 (Tremblrel. 13, last sequence update)		
DT	01-MAR-2002 (Tremblrel. 20, last annotation update)		
DE	Soluble guanylyl cyclase alpha subunit.		
OS	Oryzias latipes (Medaka fish).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;		
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;		
OC	Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.		
OX	NCBI_TaxID=8090;		

[illegible]

Dh	356	IIIRKRGVETDNTGKPMHLAGMIIYVPSNAILFLGSPCYDKLEELBGRSLYLSDIPIH	415
Qy	407	NALRDVYLIGEOARADGILKRLGLKATLEQAHQALEEEKKATVYDLCSIFPCEVAQOL	466
Dh	416	NALRDVYLIGEOAKADGILKRLGAKKALEHAHQALEEEKKATVYDLCSIFPPTVAQOL	475
Qy	467	MGOVVOAKKFSNVMTLFSIDIVGFAIACSOCSPLOVITMLALTYRFPDOCGELDYKVE	526
Dh	476	MGOETVOAKKENQVMTLFSIDIVGFAVCSLCTPMQVITMLNELYTKRFDYQCGELDYKVE	535
Qy	527	TIGDACVAGGILHKSIEDTHAVOIALMALKKMELSPENWSPHGEIYIKRIGLHSSVYAGV	586
Dh	536	TIGDACVAGGILHRESITHAVIATMALKKMELSEVTLFPGEIYIOMKIGLHSSVYAGV	595
Qy	587	VGVKMRVYLCFGNNVTLANKFESCSVPRKINVSPTTYRLKDCGFYTFPRSEELPPNF	646
Dh	596	VGVKMRVYLCFGNNVTLANKFESCSQPRKINISPTTHRYLKGPREFYVIPSRSQDLPPNF	655
Qy	647	PSEIPIGICHPLDA	659
Dh	656	PEDIPBGVCYFLFS	668

RESULT	ID	PRELIMINARY;	PROT;	678 AA.
6	P79997			
AC	P79997			
DT	01-MAY-1997 (TREMBLrel. 03, Created)			
DT	01-MAY-1997 (TREMBLrel. 03, Last sequence update)			
DT	01-MAY-2002 (TREMBLrel. 20, Last annotation update)			
DE	Soluble guanylyl cyclase alpha subunit (EC 4.6.1.2).			
OS	Oryzias latipes (Medaka fish).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;			
OC	Acanthomorphi; Acanthopterygii; Perccomorphi; Atherinomorpha;			
OC	Belontiiformes; Adriantichthyidae; Oryziinae; Oryzias.			
OX	NCBI_Taxid=8090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE-98237571; PubMed-9578459;			
RA	Mikami T., Kusakabe T., Suzuki N.;			
RT	"Molecular cloning of cDNAs and expression of mRNAs encoding alpha and			
RT	beta subunits of soluble guanylyl cyclase from medaka fish Oryzias			
RT	latipes".;			
RL	Eur. J. Biochem. 253:42-48(1998).			
DR	EMBL: AB000849; BAA19198.1; -.			
DR	HSSP: P19687; 1AMN.			
DR	InterPro: IPR001054; G_cyclase.			
DR	Pfam: PF00211; guanylate_cyc; 1.			
DR	SMART: SM00044; CYCC; 1.			
DR	PROSITE: PS00452; GUANYLATE_CYCLASES_1; 1.			
DR	PROSITE: PS50125; GUANYLATE_CYCLASES_2; 1.			
KW	lysase.			
SC	SEQUENCE 678 AA; 75133 MW; 3A6141D2A6475D40 CAC64;			
Query Match	55.9%; Score 2009.5; DB 13; Length 678;			
Best Local Similarity	59.6%; Pred. No. 7e-149;			
Matches 401; Conservative 101; Mismatches 152; Indels 19; Gaps 8;				
QY	1 MFCKRLKLDKRTGSCPSLSLARQGVPPNSESSEAGSSSCATAYPICDIDPEKNTQESLP 60			
DB	1 MFCKKLELKLKSGCPSSSAKN--NELGDFEVRSSDAAD-SLPISSDVHGK-IREWVP 55			
QY	61 QKRSRSRYVLTAEISICKLPEPEFELNVALOR--TLAKHKIKESKSL-----ERE 112			
DB	56 KQKRSRAKVNLIHTGDSIRKLACGFQRLHDLQRMATLADHSKDSSTSLHCHYQSCS 115			
QY	113 DFKETIAEQ---AVAAGVPVEVTKESIGEEVFRCYCEDENILQVVGGLTKDPLNFSPT 168			
DB	116 DKRHLVDMMKSYSTKTAIPNEALKIALGEEIFSKCYEEDGHILRYVGALHDFLNSFN 175			
QY	169 LKQSSHCQERGKRGRLSDSISILDLQEDDFLHAYYFFPKRTTSLILPGITKAANHVLYE 228			

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Db 176 LKSSMLPSDREDCVNEPSVLCIDDPGLITVYFNPSPTEFEPGVKAAACLIYN 235
Qy 229 TEVEVSIMPCFHNDCSEFNQPYLLYSVHAKSTRP-SLSPKQPSLVIPTSLFCKTTP 287
Db 236 TTYVADPLSKSDSIQSSPQSLATVYVAKAKTLSPSLRATSAQTLFTSLFTFP 295
Qy 288 FHFEPKDMITLQFGNGIRLRMRD-FQKPNFEYFELLTPKINOTSGIMTMNQF 346
Db 296 FHLIDDDLVVQGHGRKRLTRKDGRLRSPTEQHEHSIVSPQIKCTFCGLTMNLQF 355
Qy 347 VVRVRMDNSVKKSRVMDLKGOMIYVESAILFLGSPCYDRLEDFTGRGLYSDPIH 406
Db 356 IIRKHGEVTDNKGKPMDLKGOMIYVESAILFLGSPCYDRLEDFTGRGLYSDPIH 415
Qy 407 NALMDVVLIGEOARADGLKRLKATLEQAHAQALEEKKRTVDLLCSIFPCEVAOL 466
Db 416 NALMDVVLIGEOARADGLKRLKATLEQAHAQALEEKKRTVDLLCSIFPCEVAOL 475
Qy 467 WQGVVQAKKFSNTMLFSDIVGFTALCSQCSPLQVITMLALYTRDQCGGLDYKVE 526
Db 476 WQGVVQAKKFSNTMLFSDIVGFTALCSQCSPLQVITMLALYTRDQCGGLDYKVE 535
Qy 527 TIGDAYCAGGLHESDTHAVOIALMALKMMELSDVMSPHGEPDKMRIGLHSGSVFAV 586
Db 536 TIGDAYCAGGLHESDTHAVOIALMALKMMELSDVMSPHGEPDKMRIGLHSGSVFAV 595
Qy 587 VGVKMPRYCLFGNNVTLANKEFSCSVPRKINVSPTTYRLKDCPGVFTPRSRRELPP 646
Db 596 VGVKMPRYCLFGNNVTLANKEFSCSVPRKINVSPTTYRLKDCPGVFTPRSRRELPP 655
Qy 647 PSEIPIGICHLDA 659
Db 656 PEDIPGVCTFLEA 668

RESULT 7
Q90VV5 PRELIMINARY: PRT: 675 AA.
AC Q90VV5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Soluble guanylyl cyclase alpha subunit.
GN FRCS-ALPHA1.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percomorphi; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RA Morinaga C., Yamamoto T., Moriya Y., Suzuki N.;
RT "Identification of tandem organization of soluble guanylyl cyclase
RT alpha and beta subunit genes in the Japanese pufferfish (fugu
RT rubripes) genome."
RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB062171; BAB60907.1; -
DR EMBL; AB062169; BAB60905.1; -
DR InterPro: IPR001054; G_cyclase.
DR Pfam: PF00211; guanylate_cyc; 1.
DR PROSITE: PS00452; GUANYLATE_CYCLASES_1; UNKNOWN_1.
DR PROSITE: PS50125; GUANYLATE_CYCLASES_2; 1.
SQ SEQUENCE 675 AA; 75498 MW; E71A283DC0369601 CRC64;

Query Match 55.8%; Score 2005; DB 13; Length 675;
Best Local Similarity 60.1%; Pred. No. 1.6e-148;
Matches 406; Conservative 96; Mismatches 147; Indels 26; Gaps 9;
Qy 1 MFCRLKDLKLTGCGPSILA-PCGVNSESSEAGSSESCATVPICODIPKKNIQSL 59
Db 1 MFCRLKDLKLTGCGPSILA-PCGVNSESSEAGSSESCATVPICODIPKKNIQSL 53

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Qy 60 PQRSTSRVYLHTLAESICRLIPPEERLNVALQRTLAKK-----IKESRK 107
Db 54 PHOKSSRAKVMILHTGESIRKLACPEFERLHTLRMRRLSDPSRENASPVCCETEGRC 113
Qy 108 SLEREDFKITAEQAVAGVPEVYIKESGVEVKICYEEDNLCVGVGLKDFLNSF 167
Db 114 SDDPEHFVKMMSMRRAIMQDLRALGELFNMCCYEDRHILRVGGALHFLNSFN 173
Qy 168 TLKSSQCGAGKGRLEDASIIICLDEKDEPLHYIYFPPKRTSLIAGIITKAAYLY 227
Db 174 VLLKQSLHTAQDREDCVNEPSVLCIDDPGLITVYFNPSPTEFEPGVKAAARLY 233
Qy 228 TEVEVSIMPCFHNDCSEFNQPYLLYSVHAKSTRP-SLSPKQPSLVIPTSLFCKT 285
Db 224 HTTYVADPLSKSDSIQSSPQSLATVYVAKAKTLSPSLRATSAQTLFTSLFTFP 292
Qy 286 FHFEPKDMITLQFGNGIRLRMRD-FQKPNFEYFELLTPKINOTSGIMTMNQF 344
Db 293 FHLIDDDLVVQGHGRKRLTRKDGRLRSPTEQHEHSIVSPQIKCTFCGLTMNLQF 352
Qy 345 QFVVRMDNSVKKSRVMDLKGOMIYVESAILFLGSPCYDRLEDFTGRGLYSDPIH 404
Db 353 QFIRIKRGVSTA--DNTLMDLKGOMIYVESAILFLGSPCYDRLEDFTGRGLYSDPIH 410
Qy 405 IHNALRDVVLIGEOARADGLKRLKATLEQAHAQALEEKKRTVDLLCSIFPCEVAO 464
Db 411 IHNALRDVVLIGEOARADGLKRLKATLEQAHAQALEEKKRTVDLLCSIFPCEVAO 470
Qy 465 QLMGQVQAKKFSNTMLFSDIVGFTALCSQCSPLQVITMLALYTRDQCGGLDYK 524
Db 471 QLMGQVQAKKFSNTMLFSDIVGFTALCSQCSPLQVITMLALYTRDQCGGLDYK 530
Qy 525 VETIGDAYCAGGLHESDTHAVOIALMALKMMELSDVMSPHGEPDKMRIGLHSGSVFA 584
Db 531 VETIGDAYCAGGLHESDTHAVOIALMALKMMELSDVMSPHGEPDKMRIGLHSGSVFA 590
Qy 585 GVGKMPRYCLFGNNVTLANKEFSCSVPRKINVSPTTYRLKDCPGVFTPRSRRELPP 644
Db 591 GVGKMPRYCLFGNNVTLANKEFSCSVPRKINVSPTTYRLKDCPGVFTPRSRRELPP 650
Qy 645 NPPSEIPIGICHLDA 659
Db 651 NPPSEIPIGICHLDA 665

RESULT 8
Q77105 PRELIMINARY: PRT: 699 AA.
AC Q77105;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Soluble guanylyl cyclase alpha-1 subunit.
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Sphingioidea; Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98409773; PubMed=9736646;
RA Nighorn A., Gibson N.J., Rivers D.M., Hildebrand J.G., Morton D.B.;
RT "The nitric oxide-cGMP pathway may mediate communication between
RT sensory afferents and projection neurons in the antennal lobe of
RT manduca sexta."
RL J. Neurosci. 18; 7244-7255 (1998).
DR EMBL; AF062750; AAC61263.1; -
DR HSSP: P19687; IAWN.
DR InterPro: IPR001054; G_cyclase.
DR Pfam: PF00211; guanylate_cyc; 1.
DR SMART: SM00044; CYC; 1.
DR PROSITE: PS00452; GUANYLATE_CYCLASES_1; 1.
DR PROSITE: PS50125; GUANYLATE_CYCLASES_2; 1.

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KM Lyase 699 AA; 78490 MW; 989F8067ABAF8465 CRC64;
SQ SEQUENCE

Query Match 30.5%; Score 1097; DB 5; Length 699;
Best Local Similarity 37.6%; Pred. No. 2,5e-77;
Matches 266; Conservative 130; Mismatches 262; Indels 50; Gaps 19;

15 CPE-----SLAPGVNPNSSBAAGSSSCATVPICOD-----IPKNIQSLPQK 63
DB 3 CPERRASOHOFGANGSSAPAKKPEFRSRSSVHLTGEEEDGRNLTLLHMSAL-QLL 61

64 TSSRYVLTHTLASSICKLIPPEFERLNVALQRTLANHKKIESKSLEREDEFTIAQAV 123
DB 62 TASSNCLHAAYTSLTRKNSDTHKYN-----CLRLPDVYKCNNAVYLAQETDAVR 114

124 AA-GVEVEVKEISLGEVEFKICEED---ENILVVGGLTKDLPLNSFTLLKSSHQEA 179
DB 115 ATDSVNTKDFMATLGYLILITANSHNCRLERAKCGLTNLETLTIDS-VHYVLDHDT 173

180 G-KRGKLE-DASTLCDEDEDLHAYFFPKRTSLILPGIIKAAAHVLEYEVEVSLMP 237
DB 174 PLKDETFMEYEAANVCTTSGEKGKIQHLHTESEPVAVYLSLAKAKRLDYDTQDIRL- 232

238 PCFHNDCSEFVNPPLYLSV--HMKSTR-----PCLSPKPOSSIVIPISLCKPT 286
DB 233 -STNDPRPR--RYELINAVPLHOKSKESCELVNENASAVSTKVTDLKIGVASCKAR 288

287 PEHFMEDKMTILLOFGNGIRLNNRDFQKPNFEVEFFELTPK-INQPSGIMTMLMQ 345
DB 289 PMHFTDKRELVLQAGFMRLLFGTLHATGSSLSGLGYFRLRRGVPLDRREILKRNTP 348

346 FVYVRVRMNSVAKSSRWDLKCOMIYVSSAILLEGSCVRLDEFTGRLGYLSLDP 405
DB 349 FMECLMPSTALAE--LEIKQWFCESDSLELTLGSLTGLRGLGFISDPL 406

406 HNALRDVYLIGQARADGKTRKRLKATLEQAHQALBEKKKYVDLCSIPCEAAQ 465
DB 407 HMDTRVILVGEARADGKRRMDKKNIEBASAVDKERKNVSLHLIFPPHAKR 466

466 LMGOVVOAKKFSNMTLSFSDIVGTAIGSCSPLOYITMLALYFRDQCGCELDPYKY 525
DB 467 LMTGEKIEAKSHDVMLEFSDIYFTSICATAPMVIALLELDLYSVDIFCELDYKY 526

526 ETIGDAYVAGGLKHSDFPAVOIALMALKMLSDSVMSPHDEPIKMRIGLSSGVAC 585
DB 527 ETIGDAYVAGGLKHSDFPAVOIALMALKMLSDSVMSPHDEPIKMRIGLHTGYLAG 586

586 VVGKMPRYCLFNGNNTLANKEFSCSVPRKINSPTTYRLKDCPGFVTPRSRELPN 645
DB 587 VVGKMTLKYCLFNGNNTLANKEFSSGSEPLKINSPTTYEMLIKPFGDMRRDRSLPNS 646

646 FPESEIGICHFLDAY-OQGTN-SKPCFOKKDVEDGNANF-LGRASGID 690
DB 647 FPEIDIGTCYFLHAKYHPGTDPEP--QVNHIREALKDYGIQGANSTD 692

RESULT 9
Q24085 PRELIMINARY; PRT; 676 AA.
ID Q24085
AC Q24085;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE GYCALPHA99B protein.
GN GYC-ALPHA-99B OR GYCALPHA99B OR DGCA1 OR CG1912.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;

RX MEDLINE-20196006; PubMed-10731132;
RA Adams M.D., Cealiner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazet R.G., Champe M., Pfeiffer B.D.,
RA Wan R.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mikos G.L.G.,
RA Artil J.F., Agdayani A., An H.-G., Andrews-Planckoch C., Baldwin D.,
RA Bawley R.M., Basu A., Bakendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhattacharya D., Bolshakov S.,
RA Bortova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin R.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegami C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mostrel A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Wesselsbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RP [2]
RP SEQUENCE FROM N.A.
RC STRAIN-OREGON-R;
RX MEDLINE-95318108; PubMed-7797526;
RA Shah S., Hyde D.R.;
RT "Two Drosophila genes that encode the alpha and beta subunits of the
RT brain soluble guanylyl cyclase.";
RL J. Biol. Chem. 270:15368-15376(1995).
DR EMBL: AE003770; AAF56917.1; -;
DR EMBL: U27117; AA87940.1; -;
DR HSP: P19687; 1A0N;
DR Flybase: FBgn0013972; Gyc-alpha-99B.
DR InterPro: IPR001054; G_cyclase.
DR Pfam: PF00211; guanylate_cyc; 1.
DR SMART: SM00044; CYCG; 1.
DR PROSITE: P550125; GUANYLATE_CYCLASES; 2; 1.
SQ SEQUENCE 676 AA; 75662 MW; CE8097ELK3787F8 CRC64;

Query Match 27.6%; Score 991.5; DB 5; Length 676;
Best Local Similarity 37.8%; Pred. No. 4.4e-69;
Matches 247; Conservative 117; Mismatches 209; Indels 81; Gaps 20;

58 SLPORTSSRYVLTHTLASSICKLIPPEFERLNVALQRTLANHKKIESKSLEREDEFTIAQAV 159
DB 27 ALEDELSDDALTLTHQMAIOLITPNSMEDLTAVTSVAKYRQMPNHIKIKLIDPQTF 86

107 KSLEREDFEKTIAE-----QAVAGVPEVIRKESGEVEFKICEE-DENILGVYGGTL 159
DB 87 KSCANTDYIADLOELLLKMDASASBTLV-----LGEELITCCGCTIIRAFRCIGTDL 141

160 KDFLNSFS---TLKSSHCQENGKRGRLDASILCLDEDEDLHAYFFPKRTSLIP 216
DB 142 QEFISGLSDGVDTLK-----LQED-----VTDGFCVAGGGE---LIFSERPVIANMLL 189

QY	217	GIIKAAAVIETEVLEEVIMLPPCFINDCSEFNQDYLITSVH-----MKSTP-SLSPK	270
Db	190	GSIALALPMLKVDVNIKIEP--VEGDARY--RYLSVLVADNSQTMIGRPTYSKTI	244
QY	271	PO-----SSLIPTSLFCCKTPPEPHMEDKMDMTLLQFNGRIRLNMRDPQGPNF	320
Db	245	PETVQSRNSSNASDLOMNSSSFCCKMFPWHEINNEGLTELYQIGRFSKIL-----KPYM	297
QY	321	EE-----YEILLTPK-INQTFSSITMLNQPFVRRARRMDSVKKSSRWDLKGOMIT	372
Db	298	ADFGCCQATWYTFDFKRPKGLTKMFRIQVIRRTYPTPLIGLNMPGADVFAIGLEIQOMVH	357
QY	373	IVESSAIFLSPCPCVRLDEDTFGRGLYSDYIHNALRDVYLLIGQARAQDGKTRKGLT	432
Db	358	CPESNSLILFSPPLDGLDGLTGNLFESDIPLHATREVLIVGDAQARQDGLRRMDKI	417
QY	433	KATLEQAHQALEBEKKTKVDLLCSIFCEVAQOLQOGOVVAAKKFSNWTMLFSDIVGFTA	492
Db	418	KNSLEEANSATVKERKKNSVLLHLTFPEIAIEKMLGSSIDAKTPDVTILFSDIVGFTS	477
QY	493	ICSQCSPLQVITMMLNALTFRPDQCGELDYKVENTIGAVCYAGGLHKESDTHAVOIALM	552
Db	478	ICSRATPMTVISMLEGLYKNDERDFEDYKVEITIGDVCYASGLHRSITDAKRVAMA	537
QY	553	ALKMELSDSEVSPHGEPIKRIKIGLHSSSVFAGVGVKRPCLFGNNVTLANKFESCSV	612
Db	538	ALKMIDACSKRITHDGEQIKRIGLHTGTVLAVGVGRKMPRYCLGHSTVIANKFESGSE	597
QY	613	PKRINVSPTTYRLKDCPGFVF--TPRSRELEPPMPFSPITG---ICHLDAIQ	661
Db	598	ALKINVSPTTDWLTKEHGEFEELQRPDPSEFLPKFEPN--PGTETCYPLESEFR	649
RESULT 10			
Q95S04			
ID	Q95S04	PRELIMINARY:	PRT: 676 AA.
AC	Q95S04		
DT	01-DEC-2001	(TREMBLrel. 19, Created)	
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)	
DT	01-MAR-2002	(TREMBLrel. 20, Last annotation update)	
DE	GH08311P.		
GN	GYC-ALPHA-99B OR GYC-ALPHA99B OR CG1912.		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
CC	Ephydroidea; Drosophilidae; Drosophila.		
XX	NCBI_TaxID=7227;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=BERKELEY;		
RA	Stapleton M., Brockstein P., Hong L., Agbayani A., Carlson J.,		
RA	Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,		
RA	Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,		
RA	Nunoo J., Pacle J., Paragas V., Park S., Phouanavong S., Wan K.,		
RA	Yu C., Lewis S.E., Rubin G.M., Celisner S.,		
RL	Submitted (Oct-2001) to the EMBL/GenBank/DBD databases.		
DR	EMBL; AY006064; AAL28202.1; -		
DR	FLYbase; FBgn0013972; GYC-alpha-99B.		
DR	InterPro: IPR001054; G_cyclase.		
DR	Pfam: PF00211; guanylate_cyc; 1.		
DR	PROSITE: PS0125; GUANYLATE_CYCLASES_2; 1.		
SO	SEQUENCE 676 AA: GB9183E1EC314138 CRC64;		

Query Match	27.48;	Score 985.5;	DB 5;	Length 676;
Best Local Similarity	37.68;	Pred. NO. 1.3e-68;		
Matches 246;	Conservative 117;	Mismatches 210;	Indels 81;	Gaps 20

QY 58 SLPOKRTSRKRYLHTLAEISCKLTPPEERLNVALQRIPLAK-----HKRK-----ESR 106

Db 27 ALEDELDDALTLHLQWAIQLTAPSNEDNLNTAVTSVAKYRQNPINHIKRLKLDPOTF 86

QY 107 KSLREDEDEKTIAE-----QAVAAQVPPEVAKESLGEVEFKCYDE-DENILGVGGTL 159

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Db      87 K$CANVDYIADIQ$ELLKMD$AS$EILY-----L$EBELLTCCCT$IIERRARCL$TDL 141
QY      160 KDFL$N$F$---TLLKQ$SHCQ$AGKRGLEAD$A$ILCDKDEDFL$HYFFPKRT$S$ILP 216
Db      142 Q$EFL$G$LDGVY$VLK-----LQ$EED$---V$TQ$G$VC$AGE$E$---L$FT$SER$PI$AM$LL 189
QY      217 GI$K$A$A$H$Y$LE$Y$E$V$S$LM$P$C$F$IN$D$S$E$R$V$N$O$P$Y$LL$V$H$-----M$K$T$P$-S$LS$P$K 270
Db      190 G$SLK$AL$TR$M$Y$K$V$D$V$N$IK$E$P$---V$E$G$D$A$R$Y$---R$Y$E$S$LV$K$ON$S$Q$TM$LG$R$P$V$S$K$T 244
QY      271 P$Q$-----S$LV$P$T$E$C$K$T$F$P$H$E$M$D$K$M$T$L$O$G$N$IR$R$LM$NR$D$O$G$P$N 320
Db      245 P$E$Y$O$A$N$S$N$S$A$D$LO$M$N$S$S$C$K$K$F$P$H$E$T$IM$E$D$E$LE$Y$O$G$R$F$S$T$Y$-----K$P$Y 297
QY      321 E$E$-----Y$E$LL$P$K$-I$N$Q$T$S$G$IM$T$M$N$Q$F$Y$R$V$R$W$D$N$S$Y$K$K$S$R$Y$M$D$K$G$M$Y 372
Db      298 A$D$G$C$O$A$T$Y$P$E$F$K$R$K$G$L$M$K$F$R$D$V$R$Y$T$P$FL$IG$LN$P$P$G$A$D$P$P$A$IG$E$IK$G$M$H 357
QY      373 I$V$E$S$A$IL$T$G$P$C$V$D$R$L$E$D$F$T$G$R$L$Y$S$D$P$H$R$H$A$D$V$Y$LE$Q$A$R$O$D$G$K$R$G$K 432
Db      358 C$P$E$N$S$N$L$T$G$S$F$D$IG$T$G$L$C$N$E$L$F$T$D$P$H$D$A$T$E$V$Y$LE$Q$A$R$O$D$G$K$R$R$D$K$T 417
QY      433 K$A$T$E$Q$A$H$O$A$L$E$B$E$K$K$Y$D$L$C$S$IF$P$E$V$A$Q$O$L$Q$G$V$O$A$K$F$S$V$M$T$M$S$D$Y$E$T$A 492
Db      418 K$N$IE$E$A$N$S$V$Y$K$E$K$K$N$V$S$L$H$L$F$P$E$A$K$E$M$L$G$S$ID$A$K$Y$P$P$V$T$IL$F$S$D$Y$E$T$S 477
QY      493 I$C$Q$S$P$L$O$Y$T$M$L$N$A$L$Y$T$R$D$O$G$E$L$D$Y$K$V$E$T$IG$D$A$Y$C$V$A$G$L$R$E$S$D$T$H$A$V$O$T$A$L 552
Db      478 I$C$R$A$T$P$M$V$Y$S$M$L$E$G$Y$K$D$F$E$D$F$D$P$D$Y$K$V$E$T$IG$D$A$Y$C$V$A$G$S$R$A$S$Y$D$H$K$V$A$M 537
QY      553 A$L$M$M$E$L$S$D$E$V$S$P$H$E$P$Y$K$R$A$IG$H$S$G$S$Y$T$A$G$V$Y$G$V$A$M$P$R$C$L$F$G$N$N$V$T$A$N$K$E$S$C$V 612
Db      538 A$L$M$D$I$A$C$S$H$H$T$H$D$E$O$IK$M$R$IG$H$T$G$T$Y$V$A$G$V$R$E$M$P$R$C$L$G$H$S$V$T$A$N$K$E$S$G$S$E 597
QY      613 P$K$I$N$V$S$P$T$Y$R$L$K$D$C$P$E$F$V$---P$R$S$R$E$L$P$P$F$P$E$IT$G$---I$O$H$P$D$A$Y$O 661
Db      598 A$L$I$N$V$S$P$R$K$O$M$L$T$H$E$G$F$E$E$L$O$P$R$D$S$E$L$P$K$E$F$N$---P$G$E$T$C$T$F$L$E$S$R 649

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	RESULT	11
08RSJL4		
ID	Q8RSJL4	PRELIMINARY; PRF; 220 AA.
AC	Q8RSJL4	
DT	01-JUN-2002 (TREMBLrel_21, Created)	
D7	01-JUN-2002 (TREMBLrel_21, Last sequence update)	
DT	01-JUN-2002 (TREMBLrel_21, Last annotation update)	
DE	Soluble guanylate cyclase alpha2d (Fragment).	
OS	Rattus norvegicus (Rat).	
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
OX	NCBI_taxonomy=10116;	
RM	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;	
RA	Okamoto H., Asakawa T.;	
RT	"Molecular cloning of a novel variant of the rat soluble guanylate	
RT	cyclase beta2 subunit.";	
RL	Submitted (FEB-2002) to the EMBL/Genbank/DDBJ databases.	
DR	EMBL, AB079780; BAB84824.1; -.	
FT	NON_TER	1
FT	NON_TER	220
SO	SEQUENCE	220 AA; 24646 MW; DBBEC749FDAA5E35E CRC64;

Query Match 22.9%; Score 823; DB 11; Length 220;
Best Local Similarity 60.7%; Pred. No. 1.5e-56;
Matches 162; Conservative 30; Mismatches 27; Indels 48; Gaps 1;

[illegible]

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Db      61 ATFDVILVGEQAKADGCKLRKDKLAKLEKPHQALKEBKKTVDLTLSTFPGDVAQQLM 120
Oy      468 OGVOYVAKKFSNVMTLFSFDIVGFTALICGCSPLIYVITIMNALYTRFDQCGELDYKVBET 527
Db      121 QROOVQAKKFDVYTLFSDIVGFTALICGCSPLIYVITIMNALYTRFDQCGELDY---- 176
Oy      528 TGDVAVAGGLAKRESDFTHAVOIALMALKMELSDVMSPHGPIKMRIGLHSGSVAGVY 587
Db      177 -----
Oy      588 GVKMPRYCLFGNNVTYLAKFESCSYPR 614
Db      193 GVRMPRYCLFGNNVTYLAKFESGSHPR 219

RESULT 12
O90VY5 ID O90VY5 PRELIMINARY; PRT: 617 AA.
AC O90VY5.
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Soluble guanylyl cyclase beta subunit.
GN FRGS3-BETA1.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphii; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RA Morinaga C., Yamamoto T., Moriya Y., Suzuki N.;
RT Identification of tandem organization of soluble guanylyl cyclase
RT alpha and beta subunit genes in the Japanese pufferfish (Fugu
RT rubripes) genome. ";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB0621172: BAB60908.1; -
DR EMBL; AB0621170: BAB60906.1; -
DR InterPro: IPR001054; G_cyclase.
DR InterPro: IPR000834; Zn_carboxypept.
DR Pfam: PF00211; guanylate_cyc; 1.
DR PROSITE: PS00132; CARBOXYPEPT_ZN_1; UNKNOWN_1.
DR PROSITE: PS00452; GUANYLATE CYCLASES_1; UNKNOWN_1.
DR PROSITE: PS50125; GUANYLATE CYCLASES_2; 1.
SQ SEQUENCE 617 AA: 70236 MW: 785315586A06191 CRC64:

Query Match 21.9%; Score 788; DB 13; Length 617;
Best Local Similarity 34.2%; Pred. No. 3,5e-53;
Matches 202; Conservative 102; Mismatches 217; Indels 70; Gaps 15,

Oy      103 KESRSKREDREDEFEKTIQA-----VAAG-----VPVEVKESSGEEYFKICYEND-ENI 151
Db      27 READLDIEGQFLVRIYIEDATVYDLVAASVYLKIDAGDIIQLFKKFFEEFCQSGEYPTI 86
Oy      152 LGVVGGLTKDPLNSHSTLKLKSSHQCEAGKRGRLDASIIILDKR-DFLHAYYFPKRT 210
Db      87 LRVLSGNVREFLQNDAL-----HDHGLTIYPGKRAPSFRCIDAKGKSLIHYSEREG 141
Oy      211 TSLILPGTIKAAAVLYTEVEVSLMP-----CFHNDCSERVNODYLLYSVHMKSTK--- 263
Db      142 LQDVLVIGIKTVAQOHIGETLEMKTIQKSKRCDH-----IKFLIEKNSKESEA 190
Oy      264 -----PSLSPSKPOSSLVPTSPSKTPEPFHFMFKDNTIILOFGNGIRLMMNRDFOGKR 318
Db      191 FYEDLDGFEENGCTQETRISSPTT-PCAKAPFHLMPEDLDMLTQCQNALITRVQLD-PESC 248
Oy      319 NFEEYFELLTPKINQTFSGIMTLMNQFVR-----VRRMDSVYKSSRYMDLKG 368
Db      249 ILPEVFSILVRHIDFESFGILSHINTVYVLSKREGKLWVEIVENDELTVGEISCLRKG 308
Oy      369 QMTIYVSSALILFGSPCYDNLDEPFTGGLYLSDIPHNALRDVYLGEQARAQDGLKKR 428

```

ID	AC	077106	PRELIMINARY:	PRT:	600 AA.
Db					
309	QMYLPEAEMLNLFCS	PSVNMNDDLTRRGVYLSDIPLDARDVDVLVBGEQFEEKIKNOE	368		
Qy					
429	LGKLTATEQAOHQA	LEEEKKKTVDLLCSIFPCFEVAQOIHQGVYQAKKFSNTMTLFSDI	488		
Db					
369	LEILDRLQHLTHRA	LEDEKKKTRDLLRYVLPSPVAMNELHKKRPVPAKRDYNTILFSGIV	428		
Qy					
489	GFTACISCS----	PLQVITMLNALTFRFDQCGEELD---YKVFETIGDACVAGLKE	541		
Db					
429	GFNFCSHHA	SEGAIKYINLVNDVYTFRFDILITSRNNPYKYKVTGDKTYTASGLDEP	488		
Qy					
542	SDTHAVOIALMAL	KMELSDVEYMSPHGEIKMRICLHSGSVFAGVYGVMPRYCLFGNNV	601		
Db					
489	CTHNAKSTICHA	LEMLLEIAGOV-KVDDKPVQITIGIHGEVYTGIGYGRMPRYCLFGNTV	547		
Qy					
602	TLANFESC	SVPRKINVSPTTYRLLKDCPGVFETPRSEELPNNPSEIIPG	652		
Db					
548	NLTSTETTG	EGKRINVSFTRPCL-----QSAENADPQHLERYG	588		
RESULT 13					
ID	077106				
AC	077106:				
Dr	01-NOV-1998	(TREMBLrel. 08, Created)			
Dt	01-MAR-1998	(TREMBLrel. 08, last sequence update)			
Dt	01-NOV-2002	(TREMBLrel. 20, last annotation update)			
DE		Soluble guanylyl cyclase beta-1 subunit.			
OS		Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).			
OC		Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
CC		Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;			
OC		Springodea; Springidae; Springinae; Manduca.			
NCBI		taxid=7130;			
ON		[1]			
RP		SEQUENCE FROM N.A.			
RX		MEDLINE=98409773; PubMed=9736646;			
RA		Nighorn A., Gibson N.J., Rivers D.M., Hildebrand J.G., Morton D.B.;			
RT		"The nitric oxide-cGMP pathway may mediate communication between			
RT		sensory afferents and projection neurons in the antennal lobe of			
RT		Manduca sexta."			
RL		J. Neurosci. 18:7244-7255(1998).			
DR		EMBL; AF062751; AAC61264.1; -			
DR		HSSP; P16068; IAWN.			
DR		InterPro: IPR001054; G_cyclase.			
DR		Pfam: PF00211; guanylate_cyc; 1.			
DR		SMART; SM00044; CYC1.			
DR		PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.			
DR		PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.			
KW		lysase.			
SQ		SEQUENCE 600 AA; 68099 MW; 7F7D0136E6ADCB9 CRC64;			
Query Match		21.9%; Score 785.5; DB 5; Length 600;			
Best Local Similarity		33.9%; Pred. No. 5.2e-53;			
Matches 196;		Conservative 106; Mismatches 217; Indels 59; Gaps 13;			
Qy					
89	LNVALQRI	FLAAHKIKESRSL-----REFEKTIAEQAAVAGV-----PVE	130		
Db					
5	VNVALELL	VMKTFDEETWETIKKADVAMEGSFLVQIYEDETIYNLTAIVYQIQTAD	64		
Qy					
131	VIRKSLGE	EVFKICEED-ENILGVGGLTKDPLNSFSTLKKSSHCOAGRGRLDAS	189		
Db					
65	ALIEFG	TFEFCODSGDKILQVATPPDFLQNDGL-----HDHIGTLVPGMRSPS	119		
Qy					
190	ILCDK-	EDDPLHYVYFPPKRTTSLILGIIKAAAHVYETEVEVSLMPPCHNDSCSF-	247		
Db					
120	FRCTER	PDGALVHTYISDRGLEHTIVIGIKYVASKIHNTEVKEIILKTKEECHVQFL	179		
Qy					
248	-----	VQAPYLKSVNHSKTRPSLSPSKPOSSLVITPSLCKTFPFFHFMFKDMTI	298		
Db					
180	ITETST	GRVSAPELA-EIETLSLEPKSP-----ATFCRVFPFHLMDRODLNTI	227		
Qy					
239	LQFNG	IRLMLNRDFOGKPNFEFEYFELLTRKINOTSGITMLNMQFVAVRRMDSV-	357		
Db					
228	VQARV	YRSLRPRYTRPG-CRITIVLDVVRPHLETFEPAVLAHINTVYVLTKEEESVY	286		

```

OY 358 --KSSRYMDKGMITYVSSAIIFLGSPCVDRLEDTGRLYISDIPINHALDVLII 415
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 287 DPHEIASLRKGMILYPTEDVVFQCYPSVTNINDLRLGRLCIADIPLDHATDVLIM 346
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 416 GEQARADGKLRKRLGKATLEQAHQALEEKKKTVDLCSIFPEVAQOQMOGVQAK 475
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 347 SEQPEADIKLQNLQVLTQKQFFRELEEROKTDLISVLPISVAETLRRHPVAPAR 406
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 476 KFSNWTMLSDIVGFTALCSOCSS--PLQVITMLNALTFRPD--QQCGELDYKVTETI 528
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 407 RYDVITLFSIGIVGFTALCSOCSS--PLQVITMLNALTFRPD--QQCGELDYKVTETI 466
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 529 GDACVAGGLKRESPTDHAVALMALKMMELSDVMSPHGPBKIRIGLHSGSVFAGV 588
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 467 GDKYVAVSGLPEYEAHAKHISLALDMMGLS-QTVYVDSGPVIGITIGHSGEVVTGVI 525
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 589 VKMPRYCLFGNNVTLANKEFSCSVPRKINVSPTTYRL 626
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 526 HKMPRYCLFGNTVNLTRHCEFTTGVPTINVEDTYNTL 563
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 14

091XJ7 PRELIMINARY: PRT: 742 AA.

```

ID 091XJ7 PRELIMINARY: PRT: 742 AA.
AC 091XJ7
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Soluble guanylyl cyclase beta 2 subunit.
GN GUCY1B2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=KIDNEY;
RX MEDLINE=21391941; PubMed=11406623;
RA Koglin M., Vohse K., Budaus L., Scholz H., Behrends S.;
RT "Nitric Oxide Activates the beta 2 Subunit of Soluble Guanylyl Cyclase
  in the Absence of a Second Subunit."
  J. Biol. Chem. 276.30737-30743(2001).
DR EMBL; AF004153; AAF6581.1; -.
DR InterPro; IPR001054; G_cyclase.
DR InterPro; IPR001230; Prenyl_site.
DR Pfam; PF00211; guanylate_cyc; 1.
DR PROSITE; PS00452; GUANYLATE_CYCLASES_1; UNKNOWN_1.
DR PROSITE; PS0125; GUANYLATE_CYCLASES_2; 1.
DR PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
SQ SEQUENCE 742 AA; 83050 MW; 41CE148B15E244E4 CRC64;

```

Query Match 21.8%; Score 784.5; DB 11; Length 742;
 Best Local Similarity 32.6%; Pred. No. 8.5e-53;
 Matches 194; Conservative 107; Mismatches 213; Indels 81; Gaps 10;

```

OY 116 KTAAGAAAGVAVPEVETIKESIGEYFKICYED-ENILGVVGGTLKDLNFESETLKQSS 174
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 48 KLIOEACKVLDVSMELILKFGYEFKCKMSGYRMLRTLGNTLFTENLDAL----- 102
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 175 HGOEAGKRGRLSDASIIICLDEDFLHYTFPPKTTSLIIPGIIKAAAHVILEVEVYS 234
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 103 HSYTALSTQENNAVSFRVEGADGMLLHYSDRHGLHYPGITIEAAVKDFDIDVMS 162
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 235 LMPCCFHNDCEEF--NOPYLIVYHMKSTRP--SLSPKPOSS----- 274
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 163 IL-----DMNEVEERTKKEHVFLVYOKAHROLGAKASRPOSSESQADQDLQGL 216
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 275 -----LVPTSLFCKTFPPH 289
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 217 LRMRERYLNPVCPGKSHSTAVRASVLEFGKPLDFTQPVYPERLWVEEVEFCOAFPH 276
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 290 FMFKDNTIILQFGNGLRLMRNRDPOGRPNPEVEFEILLPKINQIFSGIMTLMNQFVVR 349
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

DB 277 IVFDEALNVKQAGVNIQKRYVGLITQ-KFALDEFFSIHPQVFNISICKFINSOFYTK 335
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 350 VRR-WDNSSKSSRYMDKGMITYVSSAIIFLGSPCVDRLEDTGRLYISDIPINHA 408
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 336 TREKMPARKSOPRLKIRGOMIMESLRCHIFMCSPPVNSLOLEESKMLSDIAPDPT 395
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 409 LRDVVLIGEQARADGKLRKRLGKATLEQAHQALEEKKKTVDLCSIFPEVAQOQLMQ 468
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 396 TRDILLNQORLAEMELSCQLEKKEELRVLSNHLIAETKKTETLLVAMPDEHVAHQKE 455
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 469 GQVYQAKFNSVNTMLFSIVGFTALCSOCSSPLQVITMLNALTFRPDQCGELDYKVTETI 528
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 456 GRKVAAGEFETCTILFSDVVTFTNCAACEPIQIVNLMNSMSEKDRITFSVHDYKVTETI 515
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 529 GDACVAGGLKRESPTDHAVALMALKMMELSDVMSPHGPBKIRIGLHSGSVFAGV 587
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 516 GDACVAVGVGVVYVESHQORVAVNPRALGRIKSAKEMANVTGEPIDIRIGIRGPVLAGV 575
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 588 GVKMPRYCLFGNNVTLANKEFSCSVPRKINVSPTTYRLKDCPGFVTPRSREEL 642
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 576 GDKMPRYCLFGDVTATASRMEHSGIPSKYHLSPTAHALKN-KGFEIVRGEIEV 629
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 15

054865 PRELIMINARY: PRT: 620 AA.

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ID 054865
AC 054865
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Soluble guanylyl cyclase beta-1 subunit.
GN GUCY1B3 OR GC-S-BETA-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RX Gansseman Y., Brouckaert P., Piers W.;
RA Submitted (Aug-1997) to the EMBL/Genbank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/10;
RX PubMed=10984516;
RA Sharina I.G., Krumenacker J.S., Martin E., Murad F.;
RT "Genomic organization of alpha 1 and beta 1 subunits of the mammalian
  soluble guanylyl cyclase genes."
  Proc. Natl. Acad. Sci. U.S.A. 97.10878-10883(2000).
DR EMBL; AF020339; AAB94876.1; -.
DR EMBL; AF297083; AAG17447.1; -.
DR HSSP; P16068; IAWN.
DR MGI; MGI:1860604; Gucylb3.
DR InterPro; IPR001054; G_cyclase.
DR Pfam; PF00211; guanylate_cyc; 1.
DR SMART; SM0044; CYCC; 1.
DR PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.
DR PROSITE; PS0125; GUANYLATE_CYCLASES_2; 1.
KW lysase.
SQ SEQUENCE 620 AA; 70597 MW; EED89ABF539F8E9 CRC64;

```

Query Match 21.8%; Score 781.5; DB 11; Length 620;
 Best Local Similarity 35.5%; Pred. No. 1.1e-52;
 Matches 200; Conservative 97; Mismatches 209; Indels 57; Gaps 14;

```

OY 101 KIKESKSLERDEFKTTAQAQVAVPY-----EVIKESIGEYFKICYED-ENILG 153
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 30 QLDEEGOPLVRLIYIDSDKTYDLYVAASRYLNLNAGEIL-QMKGKMFVFCQSSGYDTILR 88
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 154 VVGSTLKDFLNFSESTLKQSSHCQAGKRGRLSDASIIICLQKE-DDFLHYVYFPPKRTS 212
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 89 VLGSNVRFLQNLAL-----HDLIATYIPGRAPDSFRCTDAEKKGGLILHYISEREGIQ 143
      : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```
OY 213 LILPGIIRKAAHVLYTEVEVSIM----PCFHNDCEFWNOPLYLSVHNKSTKPS--- 265
|: ||| | : |||: | | |
Db 144 DIVGIIKTVAQOIHGTEIDMKVIAQNRNECDHTQ-----FLIEEKESKEDEFY 192
|: ||| | : |||: | | |
OY 266 -----LSPSRQSSLVIFPSLFCFTEPFPHMFEDKMTILQFGNGIRLMLNRDPQKPNF 320
|: ||| | : |||: | | |
Db 193 EDIDREFEENCTQESRISPYT-FCFAPFPHIIFDRNLVVTQCGNAIYRVLQ-PGNCSTL 250
|: ||| | : |||: | | |
OY 321 EEFYEILTPKINOTFGSMTMLNMQFVVRVRMRDMSYK-----SSRVMDLKGOM 370
|: ||| | : |||: | | |
Db 251 LSVFSLVRPHIDISFNGILSHINIVFYLRSGEGLDVEKLECEDELTGAEISCLRLKGOM 310
|: ||| | : |||: | | |
OY 371 IYIVESSAILFLGSPCVDRLEDEFTGRGLYLSDIPINALRDVYLIGQARAODGLKRLG 430
|: ||| | : |||: | | |
Db 311 IYLPENDSILFLCSPSYMNLDLTRRGLYSDIRPLHDATRDVLGEOFRREYKLTQELE 370
|: ||| | : |||: | | |
OY 431 KIKATLEQAQAALEEKKTVDDLCSIFPCEVAQAOLMOGOVQAKKFSNTMLFSDIYGF 490
|: ||| | : |||: | | |
Db 371 ILYDRLOLTLRALDEDEKKTDTLLYSVLPSPVANELRHKRPVPAKRYDNVTILFSGIYGF 430
|: ||| | : |||: | | |
OY 491 TAISQCS---PLQVITMLNALTFRPDQCGELD---YKVEITIGDAYCVAAGLHKESD 543
|: ||| | : |||: | | |
Db 431 NAFCSKHAAGEGAKIYNLNDLITRDTLDSKRNPFYIKVETVGDKMTVSGLPPECI 490
|: ||| | : |||: | | |
OY 544 THAVQIALMALKMMELSDVWSPHGEPIKMRIGLSGSVPAGVGVMPRYCFLGNVYL 603
|: ||| | : |||: | | |
Db 491 HHARSICHLALDMMELIAGV-QVDGESVQITIGIHTEGVYTGVIQRMPRYCLEGNTVNL 549
|: ||| | : |||: | | |
OY 604 ANKFESGVPRKINVSPTTYRL 626
|: ||| | : |||: | | |
Db 550 TSRETTTGEKCKINVSSETTYRCL 572
|: ||| | : |||: | | |
```

Search completed: June 27, 2003, 13:04:41
Job time : 38.7899 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2003, 13:03:32 ; Search time 14.2322 Seconds
(without alignments)
1426.467 Million cell updates/sec

Title: US-09-762-767a-2

Perfect score: 3593
Sequence: 1 MFCYKRLKDKITGECPFSL.....QKKVDENANFLKASGID 690

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCUTS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	407.5	11.3	1075	1 US-07-623-033-2	Sequence 2, Appl
2	325.5	9.1	1077	4 US-09-412-210-1	Sequence 1, Appl
3	322	9.0	1064	3 US-08-726-214-8	Sequence 8, Appl
4	319.5	8.9	1099	3 US-08-726-214-14	Sequence 14, Appl
5	319	8.9	1090	3 US-08-307-896-3	Sequence 3, Appl
6	319	8.9	1090	3 US-08-726-214-4	Sequence 4, Appl
7	319	8.9	1090	5 PCT-US95-11808-3	Sequence 4, Appl
8	303	8.4	1144	3 US-08-726-214-6	Sequence 6, Appl
9	302	8.4	1134	3 US-08-726-214-2	Sequence 2, Appl
10	299.5	8.3	533	3 US-08-726-214-18	Sequence 18, Appl
11	287.5	8.0	1253	4 US-08-864-785-2	Sequence 2, Appl
12	284.5	7.9	1248	3 US-08-726-214-16	Sequence 16, Appl
13	283.5	7.9	1098	3 US-08-726-214-10	Sequence 10, Appl
14	282.5	7.9	604	4 US-09-008-097-4	Sequence 4, Appl
15	282.5	7.9	1167	4 US-09-008-097-6	Sequence 6, Appl
16	280.5	7.8	1261	4 US-09-473-716-2	Sequence 2, Appl
17	279.5	7.8	1168	4 US-09-473-716-2	Sequence 2, Appl
18	279.5	7.8	1180	3 US-08-726-214-12	Sequence 12, Appl
19	272.5	7.6	1165	1 US-08-240-357-2	Sequence 2, Appl
20	263.5	7.3	1294	4 US-09-473-717-2	Sequence 2, Appl
21	260.5	7.3	1305	4 US-08-864-785-3	Sequence 3, Appl
22	260.5	7.3	1353	4 US-08-894-173-2	Sequence 2, Appl
23	260.5	7.3	1353	4 US-09-398-193-2	Sequence 2, Appl
24	260.5	7.3	1353	4 US-09-473-717-3	Sequence 3, Appl
25	255.5	7.1	1353	4 US-09-398-193-99	Sequence 99, Appl
26	195	5.4	670	2 US-08-997-080-178	Sequence 178, App
27	195	5.4	670	2 US-08-997-362-178	Sequence 178, App

28	195	5.4	670	4 US-09-095-855-178	Sequence 178, App
29	195	5.4	670	4 US-09-324-542-178	Sequence 178, App
30	195	5.4	670	4 US-09-205-426-178	Sequence 178, App
31	195	5.4	722	2 US-08-997-080-174	Sequence 174, App
32	195	5.4	722	2 US-08-997-362-174	Sequence 174, App
33	195	5.4	722	2 US-09-095-855-174	Sequence 174, App
34	195	5.4	722	4 US-09-324-542-174	Sequence 174, App
35	195	5.4	722	4 US-09-205-426-174	Sequence 174, App
36	192.5	5.4	107	4 US-08-857-076-76	Sequence 76, Appl
37	191	5.3	112	4 US-08-857-076-76	Sequence 76, Appl
38	187	5.2	419	2 US-08-997-080-125	Sequence 125, Appl
39	187	5.2	419	2 US-08-997-362-125	Sequence 125, Appl
40	187	5.2	419	4 US-09-095-855-125	Sequence 125, Appl
41	187	5.2	419	4 US-09-324-542-125	Sequence 125, Appl
42	187	5.2	419	4 US-09-205-426-125	Sequence 125, Appl
43	180	5.0	429	3 US-08-307-896-4	Sequence 4, Appl
44	180	5.0	429	3 PCT-US95-11808-4	Sequence 4, Appl
45	138.5	3.9	85	3 US-08-894-173-59	Sequence 59, Appl

ALIGNMENTS

```
RESULT 1
US-07-623-033-2
; Sequence 2, Application US/07623033
; Patent No. 5237051
GENERAL INFORMATION:
APPLICANT: Garbers, David L.
APPLICANT: Schultz, Stephanie
TITLE OF INVENTION: CLONING THE ENTEROTOXIN RECEPTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: TILTON, FALLON, LUNGMS & CHESTNUT
STREET: 100 South Wacker Drive - Suite 960
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60606-4002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/623,033
FILING DATE: 19901206
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: VU9018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 456-8000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1075 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-623-033-2
Query Match 11.3%; Score 407.5; DB 1; Length 1075;
Best Local Similarity 36.6%; Pred. No. 3.1e-31;
Matches 98; Conservative 47; Mismatches 94; Indels 29; Gaps 6;
QY 423 DGLKRL-----GKLTAEQAQALAEERKKTVDLCSIFCEVAQOLMOGOVQAKRS 478
DB 764 DTLIRRLQLYSRNLEHLYEERTQLYKABRDADHLNFMILPRLVYKSLKEGIVPELYE 823
QY 479 NVTMLFSDIVFTALSCSCSPLOYITMNLATRPDOCGGELDYKVTITDGYCVAGGL 538
DB 824 EVTIYFSDIVFTICKYSTPEYVMDLNDIYKSPDQIVDHHYVKKETIGDAVYVAGSL 883
```

RESULT 3
US-08-726-214-8
Sequence 8, Application US/08726214
Patent No. 6107076
GENERAL INFORMATION:
APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASIS
TITLE OF INVENTION: AND USGS THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee

RESULT 4
 US-08-726-214-14
 ; Sequence 14, Application US/08726214
 ; Patent No. 6107076
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Wei-Jen
 ; APPLICANT: Gilman, Alfred G.
 ; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
 ; TITLE OF INVENTION: AND USES THEREFOR
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee
 ; STREET: P.O. Box 4433
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: United States of America

ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,214
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: DTSD:450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1099 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-726-214-14

Query Match 8.9% Score 319.5; DB 3; Length 1099;
Best Local Similarity 26.3%; Pred. No. 1.9e-22;
Matches 82; Conservative 64; Mismatches 95; Indels 71; Gaps 8;

QY 376 SSATLFGSPCVDRLEDFGKGLYSDIPINHALRDVLLIGEQAQADGLKRLKAT 435
DB 184 ANAVTLTG-----HFTGA---FKHQLODASRDLEFY-----T 214
QY 436 LE-QAQAALBEKKKVDLCSTFPEVA-----QQLMG-----QVQA 474
DB 215 VKCJOIRKRLVERKQOENLLSVLPAHISGMKLAITERKEGDRHMPDNFHSILY 274
QY 475 KFSNVTMLFSDIYGTAFISQCSPLQVITMLNLYTRPDQCGELDYKVEITGDYCV 534
DB 275 KRQNVSLIADYIGFTRLASDCSPKELVYVNLNLFGRFDIAKANEOMRIKILGDCTYC 334
QY 535 AGGLHESDTHAVQIALMALKMEISDEYMSPHGEPIKRIGLHSGSYFAGVGVKMPRY 594
DB 335 VSGLPVSLPTHARNCYMGKLDICAIKQVREATGVDISMRYGSHGNVLCGVIGLRKQY 394
QY 595 CLEGNNTLANKEFSCVPRKINVSPTTYRL-----KDCPG-----EV 633
DB 395 DVMSHDVSILANRMEAGVPGRVHITETALNHLDRAYEVEDGEGQRPYLEKMNIRTYLV 454
QY 634 FTFRSEELPPN 645
DB 455 IDPRSQQPPPS 466

RESULT 5
US-08-307-896-3
Sequence 3, Application US/08307896C
Patent No. 6034071
GENERAL INFORMATION:
APPLICANT: Iyengar, Srinivas Ravi
TITLE OF INVENTION: MUTANT ACTIVATED GSALPHA AND ADENYLYL
TITLE OF INVENTION: CYCLASE 2 FOR USE AS THERAPEUTIC AGENTS
FILE REFERENCE: 29770
CURRENT APPLICATION NUMBER: US/08/307,896C
CURRENT FILING DATE: 1994-09-16
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 1090
TYPE: PRT

ORGANISM: Rattus norvegicus
US-08-307-896-3

Query Match 8.9% Score 319; DB 3; Length 1090;
Best Local Similarity 30.4%; Pred. No. 2.1e-22;
Matches 80; Conservative 53; Mismatches 86; Indels 44; Gaps 7;

QY 398 LYLSDIP-----IHNALRDVLLI--GEQARAQGLKRLGLKATLEQAHQ----- 441
DB 174 VYLSATGAKKHLWQILANYIIFICGLAQA---YKHL--MELAQYTRDPCNCKIS 228
QY 442 --ALEBKKTVDLCSTFPEVAQQLMGQVVO-----AKRFSN 479
DB 229 RIKLEFERKQOERILLISLPAHIAMEM-KAEIIOLOGPKAQOMENTNPNLYKRRTN 287
QY 480 VTMLFSDIYGTAFISQCSPLQVITMLNLYTRPDQCGELDYKVEITGDYCVAGVGLH 539
DB 288 VSLIYADYIGFTRLASDCSPKELVYVNLNLFGRFDIAKANEOMRIKILGDCTYC 347
QY 540 KESDTHAVQIALMALKMEISDEYMSPHGEPIKRIGLHSGSYFAGVGVKMPRYCLFGN 599
DB 348 ISLPNHAKNCYMGKLDICAIKQVREATGVDINNRVGHSGNVLCGVIGLRKQYDWSH 407
QY 600 NTLANKFSCVPRKINVSPTT 622
DB 408 DVTLANHMEAGVPGRVHISSTV 430

RESULT 6
US-08-726-214-4
Sequence 4, Application US/08726214
Patent No. 6107076
GENERAL INFORMATION:
APPLICANT: Tang, Wei-Jen
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,214
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: DTSD:450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1090 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-726-214-4

Query Match 8.9% Score 319; DB 3; Length 1090;

Best Local Similarity 30.4%; Pred. No. 2,1e-22;
Matches 80; Conservative 53; Mismatches 86; Indels 44; Gaps 7;

QY 398 LYSDIP-----IHNALRDVYL--GEQARADGLKRLGKATLEQAHO-----441
Db 174 VYLSATGAKEHLEWQILAVIIFICNLGA--YKHHL--MELALQYTRDTCIKRS 228
QY 442 --ALEEKKRTVDLCSIFPCEVAQOLMOGOVVO-----AKFSN 479
Db 229 RILFEKROERELLISLRAHIMEM-KAEIIRLOGPRAQOMENTNPHNLVYKRHTN 287
QY 480 VTMLFSDIVGFTALCSQSPLOYITMLNALYTRFDQCGELDYKVEITGDAYCAGGLH 539
Db 288 VSILYADIVGFTRLASDPSGELVHMLNELFGKFDQIAKENECMRIRKILGDCYCVSGLP 347
QY 540 KESDTHAVQIALAKRMELSDVMSPHGPPIKRIKILHSGSVFAGVYGYKMPRYCLFGN 599
Db 348 ISLPHNAKNCVKKGLDCEAIKRVKRDATGVDINMRVGHSGNYLCVIGLQKQYDVWSH 407
QY 600 NNTLANKESSVPRKINVSPTT 622
Db 408 DVTLANHMEAGVGRVHISSTV 430

RESULT 7
PCT-US95-11808-3

; Sequence 3, Application PC/TUS9511808
; GENERAL INFORMATION:
; APPLICANT: Iyengar, Sriharas Ravi V.
; TITLE OF INVENTION: MUTANT ACTIVATED GSALPHA AND
; TITLE OF INVENTION: ADENYLYL
; TITLE OF INVENTION: CYCLASE 2 FOR USE AS THERAPEUTIC AGENTS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue and
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U S.
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/11808
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,896
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Richard S.
; REGISTRATION NUMBER: 26,154
; REFERENCE/DOCKET NUMBER: 29970 165/28755
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 408-2500
; TELEFAX: (212) 765-2519
; TELEX: 650 6111063
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1090 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-11808-3

Query Match 8.9%; Score 319; DB 5; Length 1090;
Best Local Similarity 30.4%; Pred. No. 2.1e-22;
Matches 80; Conservative 53; Mismatches 86; Indels 44; Gaps 7;

QY 398 LYSDIP-----IHNALRDVYL--GEQARADGLKRLGKATLEQAHO-----441
Db 174 VYLSATGAKEHLEWQILAVIIFICNLGA--YKHHL--MELALQYTRDTCIKRS 228
QY 442 --ALEEKKRTVDLCSIFPCEVAQOLMOGOVVO-----AKFSN 479
Db 229 RILFEKROERELLISLRAHIMEM-KAEIIRLOGPRAQOMENTNPHNLVYKRHTN 287
QY 480 VTMLFSDIVGFTALCSQSPLOYITMLNALYTRFDQCGELDYKVEITGDAYCAGGLH 539
Db 288 VSILYADIVGFTRLASDPSGELVHMLNELFGKFDQIAKENECMRIRKILGDCYCVSGLP 347
QY 540 KESDTHAVQIALAKRMELSDVMSPHGPPIKRIKILHSGSVFAGVYGYKMPRYCLFGN 599
Db 348 ISLPHNAKNCVKKGLDCEAIKRVKRDATGVDINMRVGHSGNYLCVIGLQKQYDVWSH 407
QY 600 NNTLANKESSVPRKINVSPTT 622
Db 408 DVTLANHMEAGVGRVHISSTV 430

RESULT 8
US-08-726-214-6

; Sequence 6, Application US/08726214
; Patent No. 6107076
; GENERAL INFORMATION:
; APPLICANT: Tang, Wei-Jen
; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,214
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/005,498
; FILING DATE: 04-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UTSD:450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1144 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-726-214-6

Query Match 8.4%; Score 303; DB 3; Length 1144;
Best Local Similarity 30.7%; Pred. No. 8.8e-21;
Matches 84; Conservative 50; Mismatches 92; Indels 48; Gaps 9;

QY 433 KATLE-----QAHQALEEKKRTVDLCSIFPCEVAQOL-----WQGVYVOA 474
Db 253 KAFLEARQSLVEYKMLNEBQSQOQENMLSLPKRHVADEKLMKMKDESKQKQOQNTMYM 312

QY 614 KKNVSPYYRL 626
 DB 203 GRVHITKTACT 215

RESULT 11

US-08-864-785-2
 ; Sequence 2, Application US/08864/785A
 ; Patent No. 6329566
 ; GENERAL INFORMATION:
 ; APPLICANT: Kaplan, Joshua M.
 ; APPLICANT: Oppenheimer, Allison J.
 ; APPLICANT: Hitt, Anne C.
 ; TITLE OF INVENTION: METHODS FOR THE DETECTION, TREATMENT,
 ; FILE OF INVENTION: AND PREVENTION OF NEURODEGENERATION
 ; FILE REFERENCE: 00786/353001
 ; CURRENT APPLICATION NUMBER: US/08/864,785A
 ; CURRENT FILING DATE: 1997-05-29
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: FASTSEQ for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 1253
 ; TYPE: PRT
 ; ORGANISM: Caenorhabditis elegans
 US-08-864-785-2

Query Match 8.0%; Score 287.5; DB 4; Length 1253;
 Best Local Similarity 30.5%; Pred. No. 3.6e-19;
 Matches 69; Conservative 42; Mismatches 78; Indels 37; Gaps 2;

QY 439 AHQALEEKKRYVDLCISFCEVAQOLMOG----- 469
 DB 240 AKKDELETOQFDMHQSVMPKRVADKLKASSELRRPSASNSNCRSTNATQVDOPLAK 299
 QY 470 QVQAQKF-----SNVTMLFSDIVGFTALCSQSPLOYTMTALYTRFDQCGELD 521
 DB 300 MVPEKRRKRPFTMTNMTNVSILFADLAGTKMSKSKADELVNLLNDLFGREDYICRLRG 359
 QY 522 YKVTETIDGACVAGLHRESPTHAVOIALMKMELSDVMSPHGEPIKRIQLHSGS 581
 DB 360 LEKISTLDSCYCVAGCEPCDDHACRTVEGMGLDMIVIRQPDIDRGQEVNRVGIHNGK 419
 QY 582 VFAGVGVMPRYCLFGNNVTLANKEGSCVPRKINVSPTTYRLK 627
 DB 420 VMCGAVGTRKRFKDFVSDVTLANMESGVAGRVHVSATKLLK 465

RESULT 12

US-08-726-214-16
 ; Sequence 16, Application US/08726/214
 ; Patent No. 6107076
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Wei-Jen
 ; APPLICANT: Gilman, Alfred G.
 ; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
 ; TITLE OF INVENTION: AND USES THEREFOR
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee
 ; STREET: P.O. Box 4433
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: United States of America
 ; ZIP: 77210
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/726,214
 ; FILING DATE: Concurrently Herewith
 ; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/005,498
 ; FILING DATE: 04-OCT-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Highlander, Steven L.
 ; REGISTRATION NUMBER: 37,642
 ; REFERENCE/DOCKET NUMBER: UTSD:450
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (512) 418-3000
 ; TELEFAX: (512) 474-7577
 ; INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1248 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 US-08-726-214-16

Query Match 7.9%; Score 284.5; DB 3; Length 1248;
 Best Local Similarity 22.5%; Pred. No. 7e-19;
 Matches 147; Conservative 99; Mismatches 217; Indels 189; Gaps 31;

QY 103 KESRSLERDEFEKIAQAVAA--GVPVEYIKESIGEVEKICEED----- 148
 DB 568 KERNEFLKHNIEYLLINQPEBSLSLPEDIVKESV-----CSDRRNSGATTEGSWS 621
 QY 149 -----ENILG---VVGCTIKDFLNSFTLLKQSSHCQ-----EAGKGR 184
 DB 622 PELPNDIVGNQNTLAALTRNSINLPHNLQALHVGSPREINKRIEHTIDLSGDLR 681
 QY 185 LEDASILCLKEDDFL-HVY-----YFPKRTSLIDG----- 217
 DB 682 REHINPEFLMFDSSLEIKYSQMDVEFKSNLYCAFLVLLFTALQSL-LRSSRLMPTI 740
 QY 218 -----IIAAAHVLVETEVEVSIAMPCHNOCSEFVNOPYLLSYHMSSTPSPSKPQ 272
 DB 741 QESILIMHSAVLITTEDKICPLILKRCQ--WINEYIARVNIYA----- 788
 QY 273 SSVL-----IPTSLCKTFPFHFMFKDMTI--LOFGNGIRLNRDRDQKPNFEYFE 325
 DB 789 SILINFLGAVINIIMCD-----FDKSIPLKNLTFNS-----AVFTDICSYPEVF 833
 QY 326 ILTPKINTPFGIMTMAMQVVRVRNRDMSYKSSRYMDLKGMIYIVESSAI--LFL 382
 DB 834 -----VFTGVLMATVCAVFLRL---NSYLKLAVALIYA--IYALLTETIYAGLFL 879
 QY 383 GSPCYDRL-----EDFTG-----RGLYSDIPILNALRDVYLIGEOARAQDGLKRLG 430
 DB 880 S---YDNLNHSGEDPLGTRKESLILMAFLAVFH-----GQDL----- 916
 QY 431 KIKATLE-----QAQALEEK--KKTVDLCSIFCEVAQOLMO-----GOVQAQKFS 478
 DB 917 EYARLDPLMRVQAKEEINEMKDLREHNENMLRNILPHVAHFLEKDRDNELYSQYD 976
 QY 479 NYTMLEFSDIVGFTALCSQ-----SPLOYITMTALYTRFDQCGE--LDVYKVTIGDA 531
 DB 977 AVGVAFASIPGFADFTSQTENANNOGVECLIRLNLINADFLDGLDRQDIEKIKITIST 1036
 QY 532 YCVAGLHRESPT-----HAVQIALMKMELSDVMSPHGEPIKRIQLHSGSVAG 585
 DB 1037 YMAVSGLEPEKQOCEDKRGHICALADFLALTESIQEINKSFNNFEIRIGISHGCVAG 1096
 QY 586 VGVGMPRYCLFGNNVTLANKEGSCVPRKINVSPTTYRLKDCPGVFETPR 637
 DB 1097 VIGAKKPYQYDIMGKVNLANSRDSTGVGRIGVPEETYLILKD-QGFAFDPR 1147

RESULT 13

US-08-726-214-10
 ; Sequence 10, Application US/08726/214
 ; Patent No. 6107076
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Wei-Jen

APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,214
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSD:450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1098 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-726-214-10

Query Match 7.9%; Score 283.5; DB 3; Length 1098;
Best Local Similarity 26.4%; Pred. No. 7.1e-19;
Matches 83; Conservative 52; Mismatches 108; Indels 71; Gaps 8;

QY 438 QAHQALEEKKRYVDLCSTFPCVAAQL-----WGVYQAKKFSNVTMLFSDI 487
DB 253 QARHSQRENQOERLLSVLPBRVAMEMKADINAKORDMFKIYIQKHNVSTILFADI 312
QY 488 VGFPAISQCSPLQVITMNLATYTRPDQCGELDYKVEITGDAYCVAGSLHKESDTHAV 547
DB 313 EGFSLASQCTAOELVMTLNELFAFDKLAENHCLRIKILGDCYYCVSGLEPARADHAC 372
QY 548 QIALMALKMMELSDVMSPHGEPIKRIKIGLSGVFAGVGVKMPRYCLFGNNVTLANKE 607
DB 373 CCEVMGMDIMEAISVREVTGVNVMRGVSHGRCVGLGRKMQFVWSNDVTLANHM 432
QY 608 ESCGVPRKINVSPT-----YRLKDCPG-----FVF---TPRSDEL-- 642
DB 433 EAGKAGRIHITKATLNYLNGDYVEPCGGERNAVYKHSIEYFLILRQOKREERAM 492
QY 643 -----PMPFSEIPGICHFILAYQOQSTSKPCFOKK-----YVEDGNA--- 680
DB 493 IAKNNRQRTNSIGNPFRHGAERFPYNHL-----GNQVSKEMKMGFEDPKDKNADGS 546
QY 681 -----NFLGKA 686
DB 547 ANPEDVEDELGRA 560

RESULT 14
US-09-008-097-4
Sequence 4, Application US/09008097
Patent No. 6306830
GENERAL INFORMATION:
APPLICANT: Hammond, H. Kirk

APPLICANT: Insel, Paul A.
APPLICANT: Ping, Peipei
APPLICANT: Post, Steven R.
APPLICANT: Gao, Meihua
TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE
HEART FAILURE
TITLE OF INVENTION: HEART FAILURE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,097
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dylan, Tyler M.
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 22000-20567.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 604 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-008-097-4

Query Match 7.9%; Score 282.5; DB 4; Length 604;
Best Local Similarity 31.8%; Pred. No. 3.3e-19;
Matches 63; Conservative 44; Mismatches 82; Indels 9; Gaps 1;

QY 438 QAHQALEEKKRYVDLCSTFPCVAAQQLMOG-----QVYQAKKFSNVTMLFSDIV 488
DB 115 QARLHQHNRNQOERLLSVLPQHVAMEMKEDINTKEDMFKIYIQKHNVSTILFADIE 174
QY 489 GFTALCSQCSPLQVITMNLATYTRPDQCGELDYKVEITGDAYCVAGSLHKESDTHAV 548
DB 175 GFTSLASQCTAOELVMTLNELFAFDKLAENHCLRIKILGDCYYCVSGLEPARADHAC 234
QY 549 IALMALKMMELSDVMSPHGEPIKRIKIGLSGVFAGVGVKMPRYCLFGNNVTLANKE 608
DB 235 CCEVMGMDIMEAISVREVTGVNVMRGVSHGRCVGLGRKMQFVWSNDVTLANME 294
QY 609 SCGVPRKINVSPTTTRL 626
DB 295 AGSRAGRITRATLQYL 312

RESULT 15
US-09-008-097-6
Sequence 6, Application US/09008097
Patent No. 6306830
GENERAL INFORMATION:
APPLICANT: Hammond, H. Kirk
APPLICANT: Insel, Paul A.
APPLICANT: Ping, Peipei

APPLICANT: Post, Steven R.
APPLICANT: Gao, Melhua
TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE
TITLE OF INVENTION: HEART FAILURE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,097
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dylan, Tyler M
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 22000-20567.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1167 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-008-097-6

Query Match 7.9% Score 282.5; DB 4; Length 1167;
Best Local Similarity 31.8%; Pred. No. 9.9e-19;
Matches 63; Conservative 44; Mismatches 82; Indels 9; Gaps 1;
QY 438 QAHQALEEKKKTVDLCSIPCEVAQOLMOG-----QVQAKKFSNVTLFSDIV.488
DB 326 QARHLQHENRQERLLSVLPQHVAMEMKEDINTKKEDMFKIYIQKHDNVSTLFDIE 385
QY 489 GFTAICSCCSPLOYITMINALYTRPDQCCGLDVKYVETIGDAYCVAAGLHKESDTNAVQ 548
DB 386 GFTSLASQCTAQLVMTLNEFARFDKLAENHCLRIKILDCYCVSGLPEARADRAHC 445
QY 549 IALNALKMMELSDVMSPHGEPIKMRIGLHSGSVFAGVGVKMPRYCLFGNNVTLANKFE 608
DB 446 CVERKGVDTIEAISTLVREYTGVMNMRVGIHSGRVHCGVILGRKMQFDVMSNDVTLANME 505
QY 609 SCSVPRKINVSPTTYRL 626
DB 506 AGSRAGRHIHTRATLQYL 523

Search completed: June 27, 2003, 13:05:57
Job time : 16.2322 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2003, 13:05:32 ; Search time 36.3713 Seconds
(without alignments)
2080.112 Million cell updates/sec

Title: US-09-762-767a-2
Perfect score: 3593
Sequence: 1 MCTYKIKDKITGECPFSL.....QKKVEDGNANFLGKASGID 650

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 424699 seqs, 109646833 residues

Total number of hits satisfying chosen parameters: 424699

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA.*

1: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubppa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	3593	100.0	9 US-10-205-823-162	Sequence 162, App
2	3265.5	90.9	9 US-09-952-2130-2	Sequence 2, Appl
3	408.5	11.4	10 US-10-157-031-18	Sequence 18, Appl
4	408.5	11.4	10 US-09-819-249-2	Sequence 2, Appl
5	325.5	9.1	9 US-10-121-911-1	Sequence 1, Appl
6	316	8.8	10 US-10-282-942-2	Sequence 2, Appl
7	303.5	8.4	855 10 US-09-925-297-811	Sequence 811, App
8	282.5	7.9	10 US-09-750-240-4	Sequence 4, Appl
9	282.5	7.9	10 US-09-750-240-6	Sequence 6, Appl
10	280.5	7.8	1261 9 US-10-175-158-2	Sequence 2, Appl
11	279.5	7.8	1168 9 US-10-201-000-2	Sequence 2, Appl
12	279.5	7.8	1168 10 US-09-750-240-11	Sequence 11, Appl
13	278	7.7	1167 10 US-09-750-240-13	Sequence 13, Appl
14	263.5	7.3	1294 12 US-10-071-223-2	Sequence 2, Appl
15	260.5	7.3	1353 10 US-09-751-1008-2	Sequence 2, Appl
16	260.5	7.3	1353 12 US-10-071-223-3	Sequence 9, Appl
17	255.5	7.1	1353 10 US-09-751-1008-99	Sequence 99, Appl
18	212	5.9	257 9 US-09-989-442-95	Sequence 95, Appl
19	207	5.8	241 9 US-09-764-868-794	Sequence 794, App

20	207	5.8	241 9 US-09-989-442-141	Sequence 141, App
21	195	5.4	670 9 US-10-051-643-178	Sequence 178, App
22	195	5.4	670 9 US-09-880-505-178	Sequence 178, App
23	195	5.4	722 9 US-10-051-643-174	Sequence 174, App
24	195	5.4	722 9 US-09-880-505-174	Sequence 174, App
25	194	5.4	302 10 US-09-915-582-50	Sequence 50, Appl
26	192.5	5.4	107 10 US-09-205-658-76	Sequence 76, Appl
27	192.5	5.4	107 10 US-09-844-353A-76	Sequence 76, Appl
28	191	5.3	112 10 US-09-205-658-75	Sequence 75, Appl
29	191	5.3	112 10 US-09-844-353A-75	Sequence 75, Appl
30	187	5.2	419 9 US-10-051-643-125	Sequence 125, App
31	187	5.2	419 9 US-09-880-505-125	Sequence 125, App
32	181.5	5.1	311 10 US-09-925-297-515	Sequence 515, App
33	174	4.8	225 9 US-09-989-442-92	Sequence 92, Appl
34	148	4.1	109 9 US-09-764-868-795	Sequence 92, Appl
35	148	4.1	109 9 US-09-989-442-143	Sequence 143, App
36	148	4.1	109 9 US-10-091-504-1060	Sequence 1060, App
37	148	4.1	109 10 US-09-764-868-1060	Sequence 1060, App
38	138.5	3.9	85 10 US-09-751-1008-59	Sequence 59, Appl
39	137.5	3.8	85 10 US-09-751-1008-60	Sequence 60, Appl
40	137.5	3.8	85 10 US-09-751-1008-61	Sequence 61, Appl
41	133.5	3.7	85 10 US-09-751-1008-54	Sequence 54, Appl
42	133.5	3.7	85 10 US-09-751-1008-55	Sequence 55, Appl
43	133.5	3.7	85 10 US-09-751-1008-56	Sequence 56, Appl
44	133.5	3.7	85 10 US-09-751-1008-57	Sequence 57, Appl
45	133.5	3.7	85 10 US-09-751-1008-58	Sequence 58, Appl

ALIGNMENTS

RESULT 1
US-10-205-823-162
: Sequence 162, Application US/10205823
: Publication No. US20030108963A1
: GENERAL INFORMATION:
: APPLICANT: Schlegel, Robert
: APPLICANT: Monahan, John E.
: APPLICANT: Endege, Wilson O.
: APPLICANT: Gannavarapu, Manjula
: APPLICANT: Gotbachaya, Bella
: APPLICANT: Hoersch, Sebastian
: APPLICANT: Kamatkar, Shubhangt
: APPLICANT: Monsey, Angela M.
: APPLICANT: Glaty, Karen
: APPLICANT: Zhao, Xuneli
: APPLICANT: Anderson, Dustin
: TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
: TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
: FILE REFERENCE: MRI-044
: CURRENT APPLICATION NUMBER: US/10/205, 823
: PRIOR FILING DATE: 2002-07-25
: PRIOR APPLICATION NUMBER: 60/307, 982
: PRIOR FILING DATE: 2001-07-25
: PRIOR APPLICATION NUMBER: 60/314, 356
: PRIOR FILING DATE: 2001-08-22
: PRIOR APPLICATION NUMBER: 60/325, 020
: PRIOR FILING DATE: 2001-09-25
: PRIOR APPLICATION NUMBER: 60/341, 746
: PRIOR FILING DATE: 2001-12-12
: PRIOR APPLICATION NUMBER: 60/362, 158
: PRIOR FILING DATE: 2002-03-05
: NUMBER OF SEQ ID NOS: 455
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 162
: LENGTH: 690
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-10-205-823-162
Query Match 100.0%; Score 3593; DB 9; Length 690;
Best Local Similarity 100.0%; Pred. No. 1e-305;

Matches 690: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCTRLKDKLITGECFSLAPGVNNESSSEAAAGSSSSCKATVPICODIPKNIQESLP 60
 DB 1 MCTRLKDKLITGECFSLAPGVNNESSSEAAAGSSSSCKATVPICODIPKNIQESLP 60
 QY 61 ORKTSRSRVYLLHTLAESICKLIFPEPERLNAALORTLAKHKIKESRKSLEREDEKTIAE 120
 DB 61 ORKTSRSRVYLLHTLAESICKLIFPEPERLNAALORTLAKHKIKESRKSLEREDEKTIAE 120
 QY 121 QAVAGVVEVYIKESLGEVEFKICEEDENILGVVGGTLKDFLNSFTLLKQSSHCQAG 180
 DB 121 QAVAGVVEVYIKESLGEVEFKICEEDENILGVVGGTLKDFLNSFTLLKQSSHCQAG 180
 QY 181 KRGRLEDAIICLDKEDDFLHVYFFPKRTSLIPGIIKAAAHVLYETEVEVSLMPPCF 240
 DB 181 KRGRLEDAIICLDKEDDFLHVYFFPKRTSLIPGIIKAAAHVLYETEVEVSLMPPCF 240
 QY 241 HNDSEFVNOPYLLYSVHAKSTKPSLSPKPOSSLVPTSLFCKTFPPHFMFKDMTILQ 300
 DB 241 HNDSEFVNOPYLLYSVHAKSTKPSLSPKPOSSLVPTSLFCKTFPPHFMFKDMTILQ 300
 QY 301 FNGGIRRLMNRDPOGKPNFEFEELTPKINOTFSGIMTMNQFVYVRVRMDSYKKS 360
 DB 301 FNGGIRRLMNRDPOGKPNFEFEELTPKINOTFSGIMTMNQFVYVRVRMDSYKKS 360
 QY 361 SRVMDLKQMIYIYESSAILFLGSPCVRLDFTGRGLYLSDIPHNALRDVYLIGEQAR 420
 DB 361 SRVMDLKQMIYIYESSAILFLGSPCVRLDFTGRGLYLSDIPHNALRDVYLIGEQAR 420
 QY 421 AODGLKRLGKATLEBAHQALBEKKRTVDLCSIFPCVAAQOLMOGOVAAKKEFNV 480
 DB 421 AODGLKRLGKATLEBAHQALBEKKRTVDLCSIFPCVAAQOLMOGOVAAKKEFNV 480
 QY 481 TMLFSDIYGFALICSQSPLOYITMLNLYTRFDQCGELDYVYETIGDAYCAVAGLHK 540
 DB 481 TMLFSDIYGFALICSQSPLOYITMLNLYTRFDQCGELDYVYETIGDAYCAVAGLHK 540
 QY 541 ESDTHAVOIALMALKMELSDVMSPHGEPIKMRIGLHSGSVFAGVGVKMPRYCLFGNN 600
 DB 541 ESDTHAVOIALMALKMELSDVMSPHGEPIKMRIGLHSGSVFAGVGVKMPRYCLFGNN 600
 QY 601 VTLANKFSCSVPRKINVSPTTYRLKDCPGFVTPRREBLPPNFPSEIIGICHFLDAY 660
 DB 601 VTLANKFSCSVPRKINVSPTTYRLKDCPGFVTPRREBLPPNFPSEIIGICHFLDAY 660
 QY 661 QOGTNSKPCFOKKDVEDGNANFLGKASGID 690
 DB 661 QOGTNSKPCFOKKDVEDGNANFLGKASGID 690

RESULT 2
 US-09-952-213D-2
 ; Sequence 2, Application US/09952213D
 ; Publication No. US20030096240A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MURAD, FERID
 ; APPLICANT: SHARINA, IRAIDA G.
 ; APPLICANT: KROMENACKER, J. S.
 ; APPLICANT: MARTIN, E.
 ; TITLE OF INVENTION: GENOMIC ORGANIZATION OF MOUSE AND HUMAN SGC
 ; FILE REFERENCE: UTSH:252US
 ; CURRENT APPLICATION NUMBER: US/09/952,213D
 ; CURRENT FILING DATE: 2002-08-16
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 691
 ; TYPE: PRF
 ; ORGANISM: Mus musculus
 US-09-952-213D-2

Query Match 90.9%; Score 3265.5; DB 9; Length 691;

Best Local Similarity 89.6%; Pred. No. 4.8e-277;
 Matches 619: Conservative 37; Mismatches 34; Indels 1; Gaps 1;

QY 1 MCTRLKDKLITGECFSLAPGVNNESSSEAAAGSSSSCKATVPICODIPKNIQESLP 60
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 QY 61 ORKTSRSRVYLLHTLAESICKLIFPEPERLNAALORTLAKHKIKESRKSLEREDEKTIAE 120
 DB 61 ORKTSRSRVYLLHTLAESICKLIFPEPERLNAALORTLAKHKIKESRKSLEREDEKTIAE 120
 QY 121 QAVAGVVEVYIKESLGEVEFKICEEDENILGVVGGTLKDFLNSFTLLKQSSHCQAG 180
 DB 121 QAVAGVVEVYIKESLGEVEFKICEEDENILGVVGGTLKDFLNSFTLLKQSSHCQAG 180
 QY 181 KRGRLEDAIICLDKEDDFLHVYFFPKRTSLIPGIIKAAAHVLYETEVEVSLMPPCF 240
 DB 181 KRGRLEDAIICLDKEDDFLHVYFFPKRTSLIPGIIKAAAHVLYETEVEVSLMPPCF 240
 QY 241 HNDSEFVNOPYLLYSVHAKSTKPSLSPKPOSSLVPTSLFCKTFPPHFMFKDMTILQ 300
 DB 241 HNDSEFVNOPYLLYSVHAKSTKPSLSPKPOSSLVPTSLFCKTFPPHFMFKDMTILQ 300
 QY 301 FNGGIRRLMNRDPOGKPNFEFEELTPKINOTFSGIMTMNQFVYVRVRMDSYKKS 360
 DB 301 FNGGIRRLMNRDPOGKPNFEFEELTPKINOTFSGIMTMNQFVYVRVRMDSYKKS 360
 QY 361 SRVMDLKQMIYIYESSAILFLGSPCVRLDFTGRGLYLSDIPHNALRDVYLIGEQAR 420
 DB 361 SRVMDLKQMIYIYESSAILFLGSPCVRLDFTGRGLYLSDIPHNALRDVYLIGEQAR 420
 QY 421 AODGLKRLGKATLEBAHQALBEKKRTVDLCSIFPCVAAQOLMOGOVAAKKEFNV 480
 DB 421 AODGLKRLGKATLEBAHQALBEKKRTVDLCSIFPCVAAQOLMOGOVAAKKEFNV 480
 QY 481 TMLFSDIYGFALICSQSPLOYITMLNLYTRFDQCGELDYVYETIGDAYCAVAGLHK 540
 DB 481 TMLFSDIYGFALICSQSPLOYITMLNLYTRFDQCGELDYVYETIGDAYCAVAGLHK 540
 QY 541 ESDTHAVOIALMALKMELSDVMSPHGEPIKMRIGLHSGSVFAGVGVKMPRYCLFGNN 600
 DB 541 ESDTHAVOIALMALKMELSDVMSPHGEPIKMRIGLHSGSVFAGVGVKMPRYCLFGNN 600
 QY 601 VTLANKFSCSVPRKINVSPTTYRLKDCPGFVTPRREBLPPNFPSEIIGICHFLDAY 660
 DB 601 VTLANKFSCSVPRKINVSPTTYRLKDCPGFVTPRREBLPPNFPSEIIGICHFLDAY 660
 QY 661 -QOGTNSKPCFOKKDVEDGNANFLGKASGID 690
 DB 661 HQGPNKPFWDKDEEDGNANFLGKASGVD 691

RESULT 3
 US-10-157-031-18
 ; Sequence 18, Application US/10157031
 ; Publication No. US20030108890A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baranova, A. V.
 ; APPLICANT: Yanovsky, N. K.
 ; APPLICANT: Kozlov, A. P.
 ; APPLICANT: Lobashev, A. V.
 ; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequence
 ; FILE REFERENCE: 2760-103
 ; CURRENT APPLICATION NUMBER: US/10/157,031
 ; CURRENT FILING DATE: 2002-05-30
 ; NUMBER OF SEQ ID NOS: 415
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 18
 ; LENGTH: 1073
 ; TYPE: PRF
 ; ORGANISM: Homo sapiens
 US-10-157-031-18

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Query Match 11.4%; Score 408.5; DB 9; Length 1073;
Best Local Similarity 37.3%; Pred. No. 1.2e-26;
Matches 101; Conservative 43; Mismatches 92; Indels 35; Gaps 6;

OY 423 DGLKRL---GKATLEQAHQALEBKKTVDLLCSIFCEVAQAOLMOGVQAOKFS 478
      | : | | : : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 762 DTLRRRLQLYSRNLEHVEERTOLYKAERDADLNMLPLRLVYKSLKEKGFEPLE 821
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 479 NVYMLFSDIYGFETAGSCSPLOYITMNLATYRFPDQCGSLDYVYKETTIGDAVCVAGL 538
      | : | | | | | | | | : : : : | : | | | | | | | | | | | | | |
DB 822 EVYTFSDIYGFETTCIKSTIPMEVYDMLNDLYKSFDDHVDHADVKAETIGDAVVASGL 881
      | : | | | | | | | | : : : : | : | | | | | | | | | | | | | |
OY 539 HKES-DTHVAIOMALAKMELSDENVSPH--GEPFKARKIGLHSGSVFAGVGYKMPRYC 595
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 882 PKRGNRRHAIDIAKMALEILISFGTFELEDLPGLPIWIRIGVSHGPCAAGVYGIKMPRYC 941
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 596 LFGNNVYLANKEFESGVSYPKRTINVSPTTYRLKDCPGFVYTRSRDELPRNPFSEIPGCH 655
      | | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 942 LFGDTVNTASNMESTGLPLRIHVSGSTAILK-----RTE-----CQ 978
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 656 FL-----DAYOQTNRKPCFOKRDVEDGNAN 681
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 979 FLVEYRGETYLKGRGNETTYLWLTGMKDQKN 1009
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 4
US-09-819-249-2
; Sequence 2, Application US/09819249
; Patent No. US20010029019A1
; GENERAL INFORMATION:
; APPLICANT: Waldman, Scott A.
; APPLICANT: Park, Jason
; APPLICANT: Schulz, Stephanie
; TITLE OF INVENTION: Compositions And Methods For Identifying And Targeting Cancer Cells
; FILE REFERENCE: TUD2412
; CURRENT APPLICATION NUMBER: US/09/819,249
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 60/1192,229
; PRIOR FILING DATE: 2000-03-27
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1073
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-819-249-2

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RESULT 5
US-10-121-911-1
; Sequence 1, Application US/10121911
; Patent No. US20020164632A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 21529, A NOVEL ADENYLYATE CYCLASE
; FILE REFERENCE: 5800-47
; CURRENT APPLICATION NUMBER: US/10/121, 911
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US/09/412,210
; PRIOR FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1077
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-121-911-1

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Query Match          9.1%; Score 325.5; DB 9; length 1077;
Best Local Similarity 28.2%; Pred No. 2.2e-19;
Matches 91; Conservative 55; Mismatches 98; Indels 79; Gaps 9

Db      365 DLKGMIYIVESSAILFLGSPCVDRLDEPTGRLYLSIDPIHNAIDVYLIGEOARADG 424
      165 DSRPALPLQLANAVLFLGCNVA-----GVY-----HKALME-----RA----- 198
      425 LKRLGLKALKALEQA-----HQALEEKKKTVDLICSIFP-----CEVAQOLMGO 470
      199 -----LRATFREALISLSHSRRRLDTEKKHOBHLLISTILPAYLAEMKAETIARLOAQ 251
      471 -----VYQAKKESNVMTLSDDIYGFPAICSGSPLOYITMLNLTYTFEDQCGE 519
      252 GSREPTNNFHSLLYKRRHGVSVLADYIGFTPLASECPKEVLVMLNLFEGFDIAE 311
      520 LDVYEVETIGDAVYCAVAGGLHKESPDTHAVOIALMALKMLLSDEVMSPHPEPIKMRIGLS 579
      312 HECHMIKILIGDGYVCVSGPLSLPBDALINCVMGMDMCAIKRLRAATGVDDIMMRGVHS 371
      580 GSVFAGVGVKKMPRYCLEGNNVTLANKFESCSVPRKINVSPTTYRLKDC----- 639
      372 GSVLGVGVLGQMOQDVMSHDVTLTNHMEAGVGPGRVHTGTATALLAAAYAVEDAGMEH 431
      630 -----PGF-VTPPRSREE 641
      432 RDPYLRLEIGEPTLYVIDPRAEE 454

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[illegible]

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RESULT 6
US-10-282-942-2
; Sequence 2, Application US/10/282942
; Publication No. US20030087295A1
; GENERAL INFORMATION:
; APPLICANT: Silos-San'tlago, Immaculada
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITILE OF INVENTION: TREATMENT AND DIAGNOSIS OF PAIN DISORDERS USING 9805
; FILE REFERENCE: MP101-240P1RM
; CURRENT APPLICATION NUMBER: US/10/282, 942
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/335, 047
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1080
; TYPE: prt
; ORGANISM: Homo sapien
US-10-282-942-2

Query Match      8.8%;      Score 316;      DB 9;      Length 1080;
Best Local Similarity 28.2%;      Pred. No. 1,3e-18;

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	Matches	70; Conservative	53; Mismatches	85; Indels	40; Gaps	3;
Oy	438	QAHQALAEKKRKYTDLLGCSFPCCEVAQQLTMGQV-----	-YQAKES	478		
Db	217	QIRKRLRIEKKQOEWLLSVLRPAHLSMGKALAIRLEKHEGDRCPMDPNNEHSLYKRRHQ		276		
Oy	479	NVTMLFSDIVGFTALICSCQSPLOVITVLMALYTRFDQOCGELDYVKVETIGDAYCVAGGL		538		
Db	277	NVSLIADIVGFTQALDSCSPRELVVYVNETLGFKEFQJLAKANECKIRIKLGCCYCYCSGL		336		
Oy	539	HKESPTHVQVQALMALKMMELSDVEYMSHPGEPKIRIGLHSGSVYAGVGVMKPMPCYGLG		598		
Db	337	FVSLPETHARNCKVMDLMDQALIKQVREKTVGINNRVIRHSGNVLGVLGKKWQYDWS		396		
Oy	599	NNVTLANFESCSVPKRIKINSPTVYRLL-----KDCG-----	-FVETPR	637		
Db	397	HDVSLANMEAGAVGVRVHITEATLKHLDKAYEVDGHHQORDPYLKEMNIRTYLVIDPR		456		
Oy	638	SREELPPN	645			
Db	457	SCQPPPPS	464			

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1      RESULT 7
2      US-09-925-297-811
3      ; Sequence 811, Application US/09925297
4      ; Patent No. US2002081659A1
5      GENERAL INFORMATION:
6      ; APPLICANT: Rosen et al.
7      ; TITLE OF INVENTION: Nucleic acids, Proteins and Antibodies
8      ; FILE REFERENCE: PA105
9      ; CURRENT APPLICATION NUMBER: US/09/925,297
10     ; CURRENT FILING DATE: 2001-08-10
11     ; PRIOR APPLICATION NUMBER: PCT/US00/05989
12     ; PRIOR FILING DATE: 2000-03-08
13     ; PRIOR APPLICATION NUMBER: 60/124,270
14     ; PRIOR FILING DATE: 1999-03-12
15     ; NUMBER OF SEQ ID NOS: 928
16     ; SOFTWARE: PatentIn Ver. 2.0
17     ; SEQ ID NO 811
18     ; LENGTH: 855
19     ; TYPE: PRT
20     ; ORGANISM: Homo sapiens
21     FEATURE:
22     ; NAME/KEY: SITE
23     ; LOCATION: (479)
24     ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
25     ; NAME/KEY: SITE
26     ; LOCATION: (829)
27     ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
28     US-09-925-297-811

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Query Match	8.48;	Score 303.5;	DB 10;	Length 855;
Best Local Similarity	29.98;	Pred. No. 1.3e-17;		
Matches 82;	Conservative 52;	Mismatches 93;	Indels 47;	Gaps 8

[illegible]

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      |  ::  ::  |  |  ::  |
Db    230 GSRDYLE--EKIETVLIASKPEVKKTATONG 261

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RESULT 8
US-09-750-240-4

; Patent No. US20020103147A1
; GENERAL INFORMATION:
; ADDITIONAL INFORMATION:

; APPLICANT: Hammon, H. K.
 ; APPLICANT: Insel, P. A.
 ; APPLICANT: Ping, P.
 ; APPLICANT: Post, S. R.
 ; APPLICANT: Cao, W.

```

; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEARTF
; TITLE OF INVENTION: FAILURE
; FILE REFERENCE: 220002056723
;

```

;; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: US 09/472,667
PRIOR FILING DATE: 1999-12-27

PRIOR APPLICATION NUMBER: US 09/008,097
PRIOR FILING DATE 2000-01-15

;
; PRIOR FILING DATE: 1998-01-18
;
; PRIOR APPLICATION NUMBER: US 08/924,757

;; PRIOR FILING DATE: 1997-09-05
;; PRIOR APPLICATION NUMBER: US 60/048,933

PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: US 08/708,661

PRIOR FILING DATE: 1996-09-05

```
; NUMBER OF SEQ ID NOS: 13
;
; SOFTWARE: FastSeq for Windows Version 4
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; SEQ ID NO 4
; LENGTH: 604

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; TYPE: PRT
ORGANISM: Homo sapiens

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US-09-750-240-4

Query Match	7.98; Score 28
...	...

Best Local Similarity 31.8%; Pred. No
Matches 63; Conservative 44; Mismat

OV 438 OAHQALEEKKKTVDLCSIFPCVAC

115 OABY H O E H P O E P I I S V I P O U Y A M E

[illegible]

QY 489 GFTACSQCSPLQVITMNLATYTRFDQ
|||::|||::: ||::|||:

Db 175 GETSLASQCTAQELVMTLNELEFARFDKI

QY 549 IALMALKMELSDVMSPHGEPKMRIC

Db 235 CVEMGVDMIEAISLVREVTGVNVNMRVC

QY 609 SCSVPKINVSPTTYRL 626

295 AGSPRGRHTTPTATYV, 312

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RESULT 9

US-09-750-240-6
; Sequence 6, Application US/09750240

; Patent No. US20020103147A1
: GENERAL INFORMATION:

APPLICANT: Hammon, H. K.

```

; APPLICANT: INSEL, P. A.
; APPLICANT: PING, P.

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; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
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1. TITLE OF INVENTION: GENE THERAPY FOR C

FILE REFERENCE: 220002056723

;
CURRENT FILING DATE: 2001-10-12


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; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1167
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-750-240-6

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Best Local Similarity 31.8%; Score 282.5; DB 10; Length 1167;
Matches 63; Conservative 44; Mismatches 82; Indels 9; Gaps 1;

QY 438 QAHQALEEKKKTVDDLCSIFPCEVAQOLMOG-----QVYQAKKFSNTMTLPSDIY 488
DB 326 QARLHQHNRKQERLLSYLPQHVAMEKEDINTKEDMFKHTIYQKHNDVSIPLADIE 385
QY 489 GFTFATCSQSPLOVITMLNATYTRPDQCGELDYKVEITGDAYCVAGGLHKESDTHAVQ 548
DB 386 GFTSLASQCTAQAEIVMTLNEIFARFDKLAENHCLRIKLGDCYYCSGLPEARADHAHC 445
QY 549 IALMALKMELSDEWSPHGEPIKRIKIGHSVFAGVGVKMPRCLEGNNTLANKE 608
DB 446 CCEMGMDMIEALISLVREYGVNVMRGVHSGHGVGLGRKMOFVMSNDVTLANHME 505
QY 609 SCSVPRKINVSPTTYRL 626
DB 506 AGSRAGRHHITRATLOYL 523

RESULT 10
US-10-175-158-2
; Sequence 2, Application US/10175158
; Publication No. US20030008371A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, James
; APPLICANT: Cor Therapeutics, Inc.
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
; FILE REFERENCE: 44481-5027-01-US
; CURRENT APPLICATION NUMBER: US/10/175,158
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US/09/473,716
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: PCT/US98/13540
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/070,901
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/886,362
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1261
; TYPE: PRT
; ORGANISM: human type V adenylyl cyclase
; US-10-175-158-2

Query Match
Best Local Similarity 7.8%; Score 280.5; DB 9; Length 1261;
Matches 83; Conservative 52; Mismatches 108; Indels 71; Gaps 8;

QY 438 QAHQALEEKKKTVDDLCSIFPCEVAQOL-----WQGVYQAKKFSNTMTLPSDI 487

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DB 416 QARLHQHNRKQERLLSYLPQHVAMEKADINAOEDMFKHTIYQKHNDVSIPLADI 475
QY 488 GFTFATCSQSPLOVITMLNATYTRPDQCGELDYKVEITGDAYCVAGGLHKESDTHAV 547
DB 476 GFTSLASQCTAQAEIVMTLNEIFARFDKLAENHCLRIKLGDCYYCSGLPEARADHAHC 535
QY 548 IALMALKMELSDEWSPHGEPIKRIKIGHSVFAGVGVKMPRCLEGNNTLANKE 607
DB 536 CCEMGMDMIEALISLVREYGVNVMRGVHSGHGVGLGRKMOFVMSNDVTLANHME 595
QY 608 SCSVPRKINVSPTTYRL 626
DB 596 EAGGKAGRIHITATLNTLYNGDYEBPCGGERNATYKESITFTILRCTQRKKEKAM 655
QY 643 -----PNPFSSEIPGICHFIDAYQOQTSKRCPOK-----DVEDGNA--- 680
DB 656 IAKMNRQRTNSIGHNPPHMAENRPFYNH-----GQNVSKMKRKGFPDPDKAQES 709
QY 681 -----NFLGRA 686
DB 710 ANPEDEVEDEFLGRA 723

RESULT 11
US-10-201-000-2
; Sequence 2, Application US/10201000
; Publication No. US20020187540A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, James E.
; APPLICANT: Cor Therapeutics, Inc.
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
; FILE REFERENCE: 44481-5028-01-US
; CURRENT APPLICATION NUMBER: US/10/201,000
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US/09/474,076
; PRIOR FILING DATE: 1999-12-12
; PRIOR APPLICATION NUMBER: PCT/US98/13694
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/070,904
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/886,550
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1168
; TYPE: PRT
; ORGANISM: human type VI adenylyl cyclase
; US-10-201-000-2

Query Match
Best Local Similarity 7.8%; Score 279.5; DB 9; Length 1168;
Matches 63; Conservative 47; Mismatches 82; Indels 15; Gaps 2;

QY 430 GKLTATLEQAHQALEEKKKTVDDLCSIFPCEVAQOLMOG-----QVYQAKKFSN 479
DB 323 GYIQRALHQLHNRKQER-----LLSYLPQHVAMEKEDINTKEDMFKHTIYQKHNDV 377
QY 480 VTMLESDIVGFTFATCSQSPLOVITMLNATYTRPDQCGELDYKVEITGDAYCVAGGLH 539
DB 378 VSILFADIEGFTSLASQCTAQAEIVMTLNEIFARFDKLAENHCLRIKLGDCYYCSGLP 437
QY 540 KESDTHAVQIALMALKMELSDEWSPHGEPIKRIKIGHSVFAGVGVKMPRCLEGNNTLANKE 599
DB 438 EAPRADHHCCEVGVNDIEALISLVREYGVNVMRGVHSGHGVGLGRKMOFVMSNDVTLANH 497
QY 600 NVTLANKEFSCSVPRKINVSPTTYRL 626
DB 498 DVTLANHMEAGRGAGRHHITRATLOYL 524

RESULT 12

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 27, 2003, 12:42:07 ; Search time 32.6287 Seconds
(without alignments)
2527.899 Million cell updates/sec

Title: US-09-762-767a-4

Perfect score: 3231
Sequence: 1 MGFVNHALLLVIRNIGPE.....QVFLSRKNGTETKQDD 619

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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- 2: /SID2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
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- 22: /SID2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
- 23: /SID2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3231	100.0	619	21	AAV51608
2	1883	58.3	787	22	ABB58149
3	929.5	28.8	690	22	ABB60360
4	789.5	24.4	690	21	AAV70475
5	789.5	24.4	690	21	AAV51607
6	789.5	24.4	690	23	ABG61940
7	730.5	22.6	717	23	ABG61878
8	726	22.5	676	22	ABB58042
9	704.5	21.8	669	22	ABB69903
10	685	21.2	649	22	ABB69902

11	599	18.5	119	21	AA600754
12	481.5	14.9	1061	23	AAU11280
13	481.5	14.9	1061	23	AAU11281
14	481.5	14.9	1075	22	ABR11783
15	468	14.5	1029	14	AA38862
16	458	14.2	1076	22	ABR71206
17	455.5	14.1	1047	12	AA10867
18	454.5	14.1	1025	14	AA38863
19	453.5	14.0	1047	12	AA10399
20	451	14.0	1525	22	ABR71674
21	443	13.7	1076	22	ABB59684
22	429.5	13.3	566	22	ABR61743
23	429.5	13.3	975	22	ABR64661
24	407.5	12.6	1073	18	AAW32063
25	407.5	12.6	1073	19	AAW37371
26	407.5	12.6	1073	23	AAU08788
27	406.5	12.6	1172	22	ABR72034
28	404	12.5	1075	14	AA38861
29	399.5	12.4	949	22	AA383941
30	397.5	12.3	1151	22	AA383940
31	390.5	12.1	1151	22	AA383939
32	389	12.0	887	22	ABG03067
33	355.5	11.0	273	22	AA657400
34	344.5	10.7	1253	20	AA388524
35	311	9.6	1119	23	AAE17133
36	309.5	9.6	1134	21	AA302005
37	309	9.6	533	21	AA302013
38	308.5	9.5	1248	21	AA302012
39	299.5	9.3	2248	22	ABR64494
40	295	9.1	1597	22	ABR60567
41	292	9.0	1167	22	ABR58194
42	291.5	9.0	1294	20	AAW30601
43	291.5	9.0	1305	20	AAW88525
44	291.5	9.0	1353	17	AA399251
45	288	8.9	1098	21	AA302009

ALIGNMENTS

RESULT 1	AAV51608
ID	AAV51608 standard; Protein; 619 AA.
XX	
AC	AAV51608;
XX	
DT	26-MAY-2000 (first entry)
XX	
DE	Human soluble guanylylcyclase beta1.
XX	
KW	Human; guanylylcyclase alpha1; hscgbeta1; soluble;
KW	guanylylcyclase beta1; antiarteriosclerotic; vasotrophic; hypotensive;
KW	gene therapy; arteriosclerosis; restenosis; ischemia; diagnosis;
KW	peripheral arterial occlusive disease; arterial hypertension.
XX	
OS	Homo sapiens.
XX	
PN	DE19837015-A1.
XX	
PD	24-FEB-2000.
XX	
PF	14-AUG-1998; 98DE-1037015.
XX	
PR	14-AUG-1998; 98DE-1037015.
XX	
PA	(VASO-) VASOPHARM BIOTECH GMBH & CO KG.
XX	
PI	Schmidt H, Zabel U, Poller W;
XX	
DR	WPI; 2000-184044/17.
DR	N-PDB; AA28939.
XX	
PT	New human soluble guanylate cyclase alpha1/beta1 and the nucleic acid

PT encoding the subunits, useful for producing diagnostic antibodies, and
 PT for somatic gene therapy of arteriosclerosis

XX Example 1; Page 16-17; 44pp; German.

CC This invention describes novel purified human soluble guanylate cyclase
 CC alpha1/beta1 (hgcalpha1/beta1). The products of the invention have
 CC antiarteriosclerotic, vasotropic and hypotensive activity. Nucleic acid
 CC sequences encoding the alpha1 and/or beta1 subunit are useful for somatic
 CC gene therapy of arteriosclerosis and restenosis, ischemia (infarct),
 CC peripheral arterial occlusive disease and arterial hypertension.
 CC Antibodies to hgcalpha1/beta1 can be used for diagnosis of aberrant
 CC hgcalpha1/beta1 expression in human tissues. This sequence represents
 CC the human soluble guanylylcyclase beta1 subunit described in the method
 CC of the invention.

XX Sequence 619 AA;

Query Match 100.0%; Score 3231; DB 21; Length 619;
 Best Local Similarity 100.0%; Pred. No. 5,4e-306;
 Matches 619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 MYGFVNHALLELVIRNTGPEWEDIKKEAQLDEEGOFVRIIYDSKTYDLVAASKVYN 60
DB 1 MYGFVNHALLELVIRNTGPEWEDIKKEAQLDEEGOFVRIIYDSKTYDLVAASKVYN 60
OY 61 LMAGEILQMFQKMFVFCQESGYDTILRVLSNVREQLQNDLALHDLATITPGMRAPSF 120
DB 61 LMAGEILQMFQKMFVFCQESGYDTILRVLSNVREQLQNDLALHDLATITPGMRAPSF 120
OY 121 RCTDAERKGLIILHYSERGLQDIYGIITKVAQOIHGFIDMKVYQORRECDHQFL 180
DB 121 RCTDAERKGLIILHYSERGLQDIYGIITKVAQOIHGFIDMKVYQORRECDHQFL 180
OY 181 IEERKEDEFDYEDLDPEENGTOESRIISPTFCAPPHIIFPRDLVYQCGNAIRYL 240
DB 181 IEERKEDEFDYEDLDPEENGTOESRIISPTFCAPPHIIFPRDLVYQCGNAIRYL 240
OY 241 POLQPGNCSLVSFSLVRPHIDISFHGILSHINTVFLRSKGLLDVKELECEDELGTGE 300
DB 241 POLQPGNCSLVSFSLVRPHIDISFHGILSHINTVFLRSKGLLDVKELECEDELGTGE 300
OY 301 ISCLRKGMIVYLPDASITFLCSPVNMDDLTRGLYLSDDPLHNTATDVLVLSGQFR 360
DB 301 ISCLRKGMIVYLPDASITFLCSPVNMDDLTRGLYLSDDPLHNTATDVLVLSGQFR 360
OY 361 EEKRLQELILDLRLQTLRALDEKKTDTLLYSVLPVSNELHKKRPVPAKRYDNV 420
DB 361 EEKRLQELILDLRLQTLRALDEKKTDTLLYSVLPVSNELHKKRPVPAKRYDNV 420
OY 421 TILFSGIVGNAPCSKASGEGAMKIVNLNDLYTRFDLTDSKRNPFYKVVETVGDXYM 480
DB 421 TILFSGIVGNAPCSKASGEGAMKIVNLNDLYTRFDLTDSKRNPFYKVVETVGDXYM 480
OY 481 TVSGLSPRCIHHARSICHLALDMEITAGOVQVDESVOITIGITGEVYVGVIGORMPRY 540
DB 481 TVSGLSPRCIHHARSICHLALDMEITAGOVQVDESVOITIGITGEVYVGVIGORMPRY 540
OY 541 CLFGNTVNLTSRTETGCKINVSERYTCLMSPENDPOFHLHNGPVMKCKKPPMQ 600
DB 541 CLFGNTVNLTSRTETGCKINVSERYTCLMSPENDPOFHLHNGPVMKCKKPPMQ 600
OY 601 VWFLSKRNTGTEETKODD 619
DB 601 VWFLSKRNTGTEETKODD 619

```

RESULT 2
 ABB58149 ID ABB58149 standard; Protein; 787 AA.
 XX AC ABB58149;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 1239.

KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.

OS Drosophila melanogaster.

PN WO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US09231.

PR 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

PA (PEKE) PE CORP NY.

PI Venter JC, Adams M, Li PMD, Myers EW,

DR WPI: 2001-656860/75.

XX N-PSDB: ABL02252.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -

PS Disclosure; SEQ ID NO 1239; 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB101840-AB101845), expressed DNA
 CC sequences (AB101840-AB101845) and the encoded proteins
 CC (AB101840-AB101845).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 787 AA;

Query Match 58.3%; Score 1883; DB 22; Length 787;
 Best Local Similarity 49.9%; Pred. No. 3.3e-174;
 Matches 371; Conservative 102; Mismatches 125; Indels 146; Gaps 7;

```

OY 1 MYGFVNHALLELVIRNTGPEWEDIKKEAQLDEEGOFVRIIYDSKTYDLVAASKVYN 60
DB 1 MYGFVNHALLELVIRNTGPEWEDIKKEAQLDEEGOFVRIIYDSKTYDLVAASKVYN 60
OY 61 LMAGEILQMFQKMFVFCQESGYDTILRVLSNVREQLQNDLALHDLATITPGMRAPSF 120
DB 61 LMAGEILQMFQKMFVFCQESGYDTILRVLSNVREQLQNDLALHDLATITPGMRAPSF 120
OY 121 RCTDAERKGLIILHYSERGLQDIYGIITKVAQOIHGFIDMKVYQORRECDHQFL 180
DB 121 RCTDAERKGLIILHYSERGLQDIYGIITKVAQOIHGFIDMKVYQORRECDHQFL 180
OY 181 IEERKEDEFDYEDLDPEENGTOESRIISPTFCAPPHIIFPRDLVYQCGNAIRYL 240
DB 181 IEERKEDEFDYEDLDPEENGTOESRIISPTFCAPPHIIFPRDLVYQCGNAIRYL 240
OY 241 POLQPGNCSLVSFSLVRPHIDISFHGILSHINTVFLRSKGLLDVKELECEDELGTGE 300
DB 241 POLQPGNCSLVSFSLVRPHIDISFHGILSHINTVFLRSKGLLDVKELECEDELGTGE 300
OY 301 ISCLRKGMIVYLPDASITFLCSPVNMDDLTRGLYLSDDPLHNTATDVLVLSGQFR 360
DB 301 ISCLRKGMIVYLPDASITFLCSPVNMDDLTRGLYLSDDPLHNTATDVLVLSGQFR 360
OY 361 EEKRLQELILDLRLQTLRALDEKKTDTLLYSVLPVSNELHKKRPVPAKRYDNV 420
DB 361 EEKRLQELILDLRLQTLRALDEKKTDTLLYSVLPVSNELHKKRPVPAKRYDNV 420
OY 421 TILFSGIVGNAPCSKASGEGAMKIVNLNDLYTRFDLTDSKRNPFYKVVETVGDXYM 480
DB 421 TILFSGIVGNAPCSKASGEGAMKIVNLNDLYTRFDLTDSKRNPFYKVVETVGDXYM 480
OY 481 TVSGLSPRCIHHARSICHLALDMEITAGOVQVDESVOITIGITGEVYVGVIGORMPRY 540
DB 481 TVSGLSPRCIHHARSICHLALDMEITAGOVQVDESVOITIGITGEVYVGVIGORMPRY 540
OY 541 CLFGNTVNLTSRTETGCKINVSERYTCLMSPENDPOFHLHNGPVMKCKKPPMQ 600
DB 541 CLFGNTVNLTSRTETGCKINVSERYTCLMSPENDPOFHLHNGPVMKCKKPPMQ 600
OY 601 VWFLSKRNTGTEETKODD 619
DB 601 VWFLSKRNTGTEETKODD 619

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QY 235 AITRYLPOLQPCNSLVSFLVPRHIDISFGILSHINTVFLRSKREGILDVKECED 294
    1:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 355 AVSRVLPRAEENCSTLEVEAIRPHLOLNFENILSHINTIYLQTRGAMS----- 406
QY 295 ELTGTEISCLRLKGMITVYLPKADSTIFLCSPTVMNLDLTRRGLYSDTFLHATRDYL 354
    :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 407 --SRHQRLRLKGMITVYLPKADSTIFLCSPTVMNLDLTRRGLYSDTFLHATRDYL 464
QY 355 LGEQFEEKKLTQLEILDLRLQTLRALDEDEKKTDTLLYSVLPSPVANELRRKRPVA 414
    1:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 465 LSEKFAEYKTLFNTLMDTKLQOTFRDLESEKOKTDRLLYSVLPSPVANELRHQRPVP 524
QY 415 KRYDNTVILFSGIVGFNAPCSKHASEGAMKIVNLNDLYTRPDTLDSKRPVYKVER 474
    1:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 525 KRDSVTLMFSGIVGFNAPCSKHASEGAMKIVNLNDLYTRPDTLDSKRPVYKVER 584
QY 475 VQDKYMTVSGLPKPCIHHAARSICHLALDMEIAGVOYVDSQVITIGITGEVYVIG 534
    1:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 585 VQDKYMTVSGLPKPCIHHAARSICHLALDMEIAGVOYVDSQVITIGITGEVYVIG 644
QY 535 QRAPRYCLFGNTVNLSTRTETGEGKINVSERYTCLMSPEKSDPQFHLHGRGPMKG 594
    1:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 645 NRPVRCLEFGNTVNLSTRTETGEGKINVSERYTCLMSPEKSDPQFHLHGRGPMKG 704
QY 595 KKEPMQVWFLSKRNT-----GTEET 614
    1:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 705 KTPMDCMWFLTRATSSILGTST 728

RESULT 3
ABB60360 standard; Protein; 690 AA.
XX ID ABB60360;
XX AC ABB60360;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 7872.
XX KM Drosophila; developmental biology; cell signalling; insecticide;
XX KW pharmaceutical.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PE 23-MAR-2001; 2001MO-US09231.
XX PR 23-MAR-2000; 2000US-191637P.
XX PR 11-JUL-2000; 2000US-0614150.
XX PA (PERE ) PE CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EM;
XX DR N-PSDB; ABL04463.
XX PT WPI; 2001-656860/75.
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX PT interactions -
XX PS Disclosure; SEQ ID NO 7872; 21pp + Sequence Listing; English.
XX CC The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX CC useful in developmental biology and in elucidating cell signalling and
XX CC cell-cell interactions in higher eukaryotes for the development of
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX CC sequences (ABL01840-ABL16175) and the encoded proteins

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CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 690 AA;
    Query Match 28.8%; Score 929.5; DB 22; Length 690;
    Best Local Similarity 34.8%; Pred. No. 3.3e-81;
    Matches 218; Conservative 129; Mismatches 231; Indels 49; Gaps 15;

QY 1 MGFVNALELLIYRNGPEWEDIKKQALDEGQFLVRIYDSDKTYDLVAASKVNLN 60
    1:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 1 MYGLLENISEYTKSYGEEKMEDIRQAGIDSP-SFSVQVYPPENILQLAKKAOVLG 59
QY 61 LNAAGELQMGKKEFFPCQESSGYDTILRVGSVNRFLQNLADLHHAITYGMRAPSP 120
    1:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 60 VSEKDFMDQNGVYFVGQYGRVLSVGRMRPFLNGLNHELFKSPMRAPSP 119
QY 121 RCTDAKRGKLLIHYSEREGQDIYIGILIKYVAQOIHGEIDMKVYQOR----- 170
    1:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 120 ICENETK-QGLTIHYSKRGFYTYMGQLEVARAFYHKEMIELVREIILDPYHYTF 178
QY 171 NEECDFQTLIEEKSEKEDYEDLDREENGQESRISPYTECKAPPHIIFRDVLVTF 230
    1:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 179 QLFEDNRAFLIASIAMTREF-----KHLPISAHVLFEIFPCMGVPGADVVYR 225
QY 231 QCGNATRYLPOLQPCNSLVSFLVPRHIDISFGILSHINTVFLRSKREGILDVKEK 290
    1:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 226 SIGNSLAVILPELL--GKTIAMFDLVRPLIARFQYILNRNINIELVYDVDTGEFV 283
QY 291 ECHDEL---TGTE-ISCLRLKGMITVYLPKADSTIFLCSPTVMNLDLTRRGLYSDIPLH 346
    1:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 284 QNEDLLQHEDESGPEKSLRLKGMVYEMNRMIFLGTVPMPRLSLITGLYINDLSM 343
QY 347 DATRDVYLGEQFEEKKLTQLEILDLRLQTLRALDEDEKKTDTLLYSVLPSPVANE 405
    1:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 344 DFRSDMLAGTQOSVELKALDQEOOKSKIEESMRDLDEEMRTDELLYQMPIKQVADR 403
QY 406 LRH-KRPV-PAKRYDNTVILFSGIVGFNAPCSKHASEGAMKIVNLNDLYTRPDTLDS 463
    1:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 404 LRGENPDIQCEMFDSILFSDIVTFTEICSKRT---PMEVSMINAAWTSFIDKITER 459
QY 464 RKNPFYKVEYVGDKTYMTVSGLPKPCIHHAARSICHLALDMEIAGVOV--VDESQVIT 521
    1:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 460 NS--YKVEYITDAAVYVAGAPDKOANHAERVCNALDMDVADITLDKDSIQGLHRIY 516
QY 522 GHTGEVYVGVICQRPRTCLFGNTVNLSTRTETGEGKINVSERYTCLMSPEKSDPQ 581
    1:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 517 GVHSGAVVAGIVGIKMPRYCLFGDYVTATSRMESTSIAMKVHISEST-KVLIG----PN 570
QY 582 FHLHGRGPMKGKKEPMQVWFLSKRN 608
    1:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 571 YKIIERGEIDYKGGTYMGLWEREN 597

RESULT 4
AAV70475
ID AAV70475 standard; Protein; 690 AA.
XX AC AAV70475;
XX DT 04-JUL-2000 (first entry)
XX DE Human cyclic nucleotide-associated protein-3 (CNP-3).
XX KM Cyclic nucleotide-associated protein-3; CNP-3; human; cytosolic;
XX KM anti-arteriosclerotic; hepatotropic; anti-leukemic; anti-inflammatory;
XX KM immunomodulatory; anti-asthmatic; anti-anemic; anti-diabetic; diagnosis;
XX KM anti-sclerotic; dermatological; neuroprotective; anti-epileptic; cancer;
XX KM anti-Alzheimer's; anti-Parkinsonian; cerebroprotective; ophthalmological;
XX KM anti-infertility; anti-allergic; vasotropic; immunosuppressive;
XX KM hypotensive; gene therapy; prevention; treatment; arteriosclerosis;

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cell proliferative disorder; autoimmune/inflammatory; diabetes mellitus;
neurological; vision; reproductive; smooth muscle.

Homo sapiens.

Key Location/Qualifiers

65 /note= "Potential phosphorylation site"
211 /note= "Potential phosphorylation site"
361 /note= "Potential phosphorylation site"
450 /note= "Potential phosphorylation site"
478 /note= "Potential phosphorylation site"
29 /note= "Potential phosphorylation site"
73 /note= "Potential phosphorylation site"
117 /note= "Potential phosphorylation site"
135 /note= "Potential phosphorylation site"
158 /note= "Potential phosphorylation site"
229 /note= "Potential phosphorylation site"
511 /note= "Potential phosphorylation site"
527 /note= "Potential phosphorylation site"
638 /note= "Potential phosphorylation site"
687 /note= "Potential phosphorylation site"
39 /note= "Potential phosphorylation site"
64 /note= "Potential phosphorylation site"
105 /note= "Potential phosphorylation site"
261 /note= "Potential phosphorylation site"
328 /note= "Potential phosphorylation site"
356 /note= "Potential phosphorylation site"
360 /note= "Potential phosphorylation site"
394 /note= "Potential phosphorylation site"
622 /note= "Potential phosphorylation site"
635 /note= "Potential phosphorylation site"
27 /note= "Potential phosphorylation site"
332 /note= "N-glycosylated"
479 /note= "N-glycosylated"
600 /note= "N-glycosylated"
472..661 /note= "N-glycosylated"

Region

/note= "Guanylate cyclase signature sequence identified by PFAM analysis: CNAP-3 shares 89% identity with human soluble guanylate cyclase large subunit."

W0200014248-A1.

16-MAR-2000.

XX 03-SEP-1999; 99WO-US20287.
XX 04-SEP-1998; 98US-0148904.
XX (INCY-) INCYTE PHARM INC.
XX Hillman JL, Yue H, Guegler KJ, Corley NC, Patterson C, Tang YT;
XX MPI; 2000-256994/22.
XX N-PSDB; AAZ51684.

Isolated cyclic nucleotide associated proteins useful for preventing, diagnosing and treating cell proliferative, autoimmune/inflammatory, neurological, vision, reproductive and smooth muscle disorders -
Di Disclosure: Page 67-69; 78pp; English.

The present sequence is a human cyclic nucleotide associated protein-3 (CNAP-3), identified in incyte clone 159278, that is isolated from ADENINB01 cDNA library. It is expressed in nervous, reproductive, cardiovascular and developmental tissues. CNAP sequences may be used for prevention, treatment and diagnosis of diseases associated with altered CNAP expression such as, cell proliferative disorders (e.g. arteriosclerosis, cirrhosis, leukaemia, lymphoma and cancer of the breast, prostate, lung and brain), autoimmune/inflammatory disorders (e.g. asthma, anaemia, diabetes mellitus, multiple sclerosis and psoriasis), neurological disorders (e.g. epilepsy, Alzheimer's/Parkinson's disease and strokes), vision disorders (e.g. conjunctivitis, glaucoma, cataracts and retinitis pigmentosa), reproductive disorders (e.g. infertility, uterine fibroids, ectopic pregnancies and impotence) and smooth muscle disorders (e.g. angina, anaphylactic shock, Kearns-Sayre syndrome and hypertension). The coding sequence can be used for gene therapy.

Sequence 690 AA:

Query Match 24.4%; Score 789.5; DB 21; Length 690;
Best Local Similarity 35.1%; Pred. NO. 1.5e-67;
Matches 207; Conservative 96; Mismatches 219; Indels 67; Gaps 15;

30 QLDEEGFLVRIITDDSKTYDVAASKVLMNGEIL-QMFGMFYFCGSESYDILR 88
101 KIKESKSLERDEDEKTIADQAVAGVP-----EVKESLGEVFRICEED-ENILG 153
89 VLGSNVEFLQNLDAI-----HDHLATYPCMRAPSEFCDAERKGLILHYSERGLQ 143
154 VVGGLKDFLNSFTLLKQSSHCQAGKRGLEDAISICLDKE-DPLHYHYFFPRRTTS 212
144 DIVGIIKTVAQQLHGFEDIMKVIQQRNECDHQ-----FLIEKESKEDFY 192
213 LILPGIILKAHVAVLYEVEVSLM---PPCFHNDGSEFVNOPYLLVSVHKSTRPS-- 265
193 EDLRFENNGQESRISPYT-FCKAPPHIFEDBDLVATQCGNAIVYLPOLQ-PGNCSL 250
266 -----LSPSKQSSLVIPSTLFCFTPPHFFEDDMITLQGNIRLMMRRDPQGPNF 320
251 LSVESLVRPHIDISFHGILSHINTFVYLSRKEGLDVEKLECEDELGTETISCLRLGOM 310
321 EEFEEILTPKINQFSGIMTLMNQFVYVRAMNSVK-----SSRVMDLKGOM 370
311 IYLEDASILFLCSPSVNDDLTFRGLYLSDIPLHATRDVLVLSGQFREFRYTQELE 370
371 IYIVESSAILFLGSPCDVRLDEDFTGRGLYLSDIPHNAIRDVYVIGDARADLKRRLG 430
371 ILTRLDLRLALDEKKTKDTLLYSVLPVANELHKKRPVPAKRDNTYILFSGIVGF 430
431 KLRATLQDAQALDEEKTKTYDLCSITPCVAAQQLQOGVOGVAKNTMTFSDIVGF 490
431 NAFCSKHASGCAKIVNLLNDLTTRFDLTDSRKNPFFYKVEIVGDKRYMTVSGILPPCI 490
491 TATSGCS---PLOYITMLNALTTRFDQCGELD---YKVEITIGAYCYAGSLHRES 543


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OY 491 HHAASICHIALDMMETAGOV-OVDGESVOITGHTGEVYVYIGQMRPRYCLFGNTVL 549
DB 544 THAVOIALMALKMEIODEVMSPHGEPIKMRIGLHSGSVFAGVYKMPRYCLFGNNVTL 603
OY 550 TSRTETGKRGKINSEYTYRCL-----MSPENDPOPHLEHRS 588
DB 604 ANKFESCSVPKRINVSPTTYRLKDCPGVFPTPRSRREELPPNPSEIPG 652

RESULT 5
AAY51607
ID AAY51607 standard; Protein; 690 AA.
XX
XX AAY51607;
XX
DE 26-MAY-2000 (first entry)
XX
XX Human soluble guanylylcyclase alpha protein.
XX
XX Human; guanylylcyclase alpha; hscGcalpha; hscGbeta; soluble;
XX guanylylcyclase beta; antiarteriosclerotic; vasotropic; hypotensive;
XX gene therapy; arteriosclerosis; restenosis; ischemia; diagnosis;
XX peripheral arterial occlusive disease; arterial hypertension.
XX
XX Homo sapiens.
XX
XX DE19837015-A1.
XX
XX 24-FEB-2000.
XX
XX 14-AUG-1998; 98DE-1037015.
XX
XX 14-AUG-1998; 98DE-1037015.
XX
XX 14-AUG-1998; 98DE-1037015.
XX
XX (VASO-) VASOPHARM BIOTECH GMBH & CO KG.
XX
XX Schmidt H, Zabel U, Poller W;
XX
XX WPI; 2000-184044/17.
XX
XX N-PSDB; AA288938.
XX
XX New human soluble guanylate cyclase alpha/beta and the nucleic acid
XX encoding the subunits, useful for producing diagnostic antibodies, and
XX for somatic gene therapy of arteriosclerosis -
XX
XX Example 1; Page 13-15; 44pp; German.
XX
XX This invention describes novel purified human soluble guanylate cyclase
XX alpha/beta (hscGcalpha/beta). The products of the invention have
XX antiarteriosclerotic, vasotropic and hypotensive activity. Nucleic acid
XX sequences encoding the alpha and/or beta subunit are useful for somatic
XX gene therapy of arteriosclerosis and restenosis, ischemia (infarct),
XX peripheral arterial occlusive disease and arterial hypertension.
XX Antibodies to hscGcalpha/beta can be used for diagnosis of aberrant
XX hscGcalpha/beta expression in human tissues. This sequence represents
XX the human soluble guanylylcyclase alpha subunit described in the method
XX of the invention.
XX
XX Sequence 690 AA;
XX
XX Query Match 24.4%; Score 789.5; DB 21; Length 690;
XX Best Local Similarity 35.1%; Pred. No. 1.5e-67;
XX Matches 207; Conservative 96; Mismatches 219; Indels 67; Gaps 15;

OY 30 QDDEGQFLVRIYDQSKTYDLVAASKVNLNAGIIL-QMFGKMFVFCQESGYDTIR 88
DB 101 KIKESRKSLEKDEFEKTIAEOAVAGVP-----EVIESIGEEVFKICYED-ENILG 153
OY 89 VLSNVREFLQNLDA-----HDHLATIPGKAPSFCTDAEKGKGLILHYYSEREGLQ 143
DB 154 VVGGLKDFLNFSTLTKQSSHQEGKRGRLDASILCLDKE-DFLHAYVFFPRRTS 212
OY 144 DIVIGIKTVAOOIHGTEIDMKVYIQQRNECHTQ-----FLIEKESKEDEPY 192

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DB 213 LILPGIKKAAAVLYETEVEVSLM-----PPCFHNDCSEFVNOPYLLYSVHMKSTRPS--- 265
OY 193 EDLDREENGQTESRISPT-FCKAFFHIIIDRDLYVQGNATYRVLPQ-IGNCSL 250
DB 266 -----LSPSKPQSSILVPTSLFCKTFPFHMFMDKMTILQFNGIRLRNRDFOGKPNF 320
OY 251 LSVFSLVRPHIDISFNGILSHINTVFLRSKGLDVERLECEDELTGEISCLRKGOM 310
DB 321 EEFFELTPKINOTFSGITMLNMQFVAVRRRDNVSK-----SRVMDLKGOM 370
OY 311 IYLPADSTLFLCSPSVNMLDITFRRLGLYLSDIPLDATRDLYLGEQFREERYKLTQGLE 370
DB 371 IYVESALLFLFSGPCVDRLEDFTGRLYSIPHNALRDVYLIGEQAADGLKRLIG 430
OY 371 ILTDRLOLTLRALDEKKTDTLLYSVLPPSVANEIRHRPAPAKYDVTITFSGIYGF 430
DB 431 KIKATLEQAHQALEEKKTVDLCSIFCEVAQQLMGQGVQAKKFSVNTLPSDIVGF 490
OY 431 NAFCSKHASGEGAMKIVNLNDLYTRFDLTDSRKNPFYKYETVGDKYMTVSGLPPECI 490
DB 491 TAIQSQCS-----PIQVITMLNLYTRFDQCGELD---YKYETIGDACYVAGGLHKESD 543
OY 491 HHAASICHIALDMMETAGOV-OVDGESVOITGHTGEVYVYIGQMRPRYCLFGNTVL 549
DB 544 THAVOIALMALKMEIODEVMSPHGEPIKMRIGLHSGSVFAGVYKMPRYCLFGNNVTL 603
OY 550 TSRTETGKRGKINSEYTYRCL-----MSPENDPOPHLEHRS 588
DB 604 ANKFESCSVPKRINVSPTTYRLKDCPGVFPTPRSRREELPPNPSEIPG 652

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RESULT 6
ABG61940
ID ABG61940 standard; Protein; 690 AA.
XX
XX ABG61940;
XX
DE 15-AUG-2002 (first entry)
XX
XX Prostate cancer-associated protein #141.
XX
XX Prostate cancer; prostate tumour tissue; human; mammal; cytosolic.
XX
XX Mammalia.
XX
XX WO200230268-A2.
XX
XX 18-APR-2002.
XX
XX 12-OCT-2001; 2001WO-US32045.
XX
XX 13-OCT-2000; 2000US-0687576.
XX 08-DEC-2000; 2000US-0733288.
XX 08-DEC-2000; 2000US-0733742.
XX 24-JAN-2001; 2001US-263957P.
XX 16-MAR-2001; 2001US-276791P.
XX 16-MAR-2001; 2001US-276888P.
XX 06-APR-2001; 2001US-281922P.
XX 24-APR-2001; 2001US-286214P.
XX 30-APR-2001; 2001US-0847046.
XX 04-MAY-2001; 2001US-288589P.
XX
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
XX
XX WPI; 2002-471335/50.
XX
XX N-PSDB; ABK92259.
XX
XX Detecting a prostate cancer-associated transcript in a cell in a
XX patient; useful for diagnosing prostate cancer (PC) or screening
XX modulators of PC, by determining if prostate cancer-associated genes
XX

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pt are expressed in a prostate tissue -

xx
xx Claim 27; Page 421-422; 436pp; English.

cc The present invention relates to methods of detecting a prostate cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer-associated polynucleotides (designated pc genes) that selectively hybridize to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissues or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals (e.g., mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer-associated genes are useful for diagnosing or treating prostate cancer, as well as for identifying modulators of prostate cancer or agents that inhibit prostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications.

cc Abg61800-Abg61944 represent prostate cancer-associated proteins.
cc
cc
cc
xx

SQ Sequence 690 AA;

Query March 24.4%; Score 789.5; DB 23; Length 690;
Best Local Similarity 35.1%; Pred. No. 1.5e-67;
Matches 207; Conservative 96; Mismatches 219; Indels 67; Gaps 15.

QY 30 QLDEGGQFLVNIYYDDSKTYDLVAASRYLMNAGEIL-QMGKMFFFCQSGDYTLIR 88
Db KIKSRKSRLERDEDEKTIADGAVAAQPV-----EVAKESLGEEVFATCYED-ENILG 153
QY 89 VLGSNVREFIIONDAL-----HDILATIYPGRAPDSFCTDAEKGKGLIHAYSEREGIQ 143
Db 154 VVGSTLDLFNLFSFTLKQSSHCCEAGRGRIELDASITCLDR-DDFLHYVYFFPKRTTS 212
QY 144 DIVIGIITVAOQJHGTFIDMKVKVIOQRNECDHQ-----FLIEEKSEEDPY 192
Db 213 LILGIITKAANHLVETREVEYSIM----PPEFHNDCSFYVQPIYLIVSNHKSTPS--- 265
QY 193 EDLDRFEENGQESRISPTT-FCKAFPHIIFDRDLVTVOCGMAIYRVLPOLQ-PGNCSL 250
Db 266 ----LSPSKPOSSVIPTSLFCCTPPHFPMFDKMOTLLQGNGCIRLRMLNRDFOGKRNF 320
QY 251 LSVSIVAPHIDISHGHLSHINPFVRSRSGLLDVKEKLCEDELDTETLSQLTKGOM 310
Db 321 EYEYIELPKINQTFSSGITMILNQGVYKVRMDNSVAK-----SSRWMLKGOM 370
QY 311 IYLPBADSIPLFCSPSVNMIDLTRRGDIYLSIDIPLHADTLDVLLEGEQFREBYKTGLE 370
Db 371 IYIYESSAILFLFGSPCVDRLEDFTGRGLYLSIDIPHNALRDVVLIGEQAARDGLKKRLG 430
QY 371 ILTPRLQUTLALADEKKKTDTLLXSVLPSPVANELRRKRPYPAKRYDNVTILBSGYGF 430
Db 431 KLKATLTDRARHALDEERKKKYDLLCSIFPCFEAQQLOMGQVQAOKKFNNVMTLSDIYGF 490
QY 431 NAFCSKSHASGGAIAVNLNDLYTRFPTLTDSCRKNPVPYKVEYTGADSYMTVSGIPPCI 490
Db 491 TALCSQGS---PLYVTIMNALVTRPDQGGELD--YIVAVETIGDAVCYAAGLHKRSD 543
QY 491 HHANSICHLADMELIAGOV-QVDGESVQITIGHTGETVTVGTGQMRPRYCLEGNVTNL 549
Db 544 THAVIDALMAKMMELSDENVSPGPBKIRIGHSGVFAVVGVKMPRCYLEGNVTNL 603
QY 550 TSTRFTTEGKGIINVSEITYRCL-----MSPEMSDQFIHEHHG 588
Db 604 ANKFSCSVPRKINVSPTTYRLRLDKDCPGVFTPPSRRELPPNFBSEIIPG 652

RESULT 7
ABG61878
1 ID ABG61878 standard; Protein: 717 AA.
XX
CC ABG61878;

XX	15-AUG-2002	(first entry)	
XX	Prostate cancer-associated protein #79.		
XX	Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.		
XX	Mammalia.		
OS	WO2002030268-A2.		
XX			
PD	18-APR-2002.		
XX			
PF	12-OCT-2001; 2001WO-US32045.		
XX			
PR	13-OCT-2000; 2000US-0687576.		
PR	08-DEC-2000; 2000US-0733288.		
PR	08-DEC-2000; 2000US-0733742.		
PR	24-JAN-2001; 2001US-263957P.		
PR	16-MAR-2001; 2001US-276791P.		
PR	16-MAR-2001; 2001US-276888P.		
PR	06-APR-2001; 2001US-281922P.		
PR	24-APR-2001; 2001US-286214P.		
PR	30-APR-2001; 2001US-0847046.		
PR	04-MAY-2001; 2001US-288589P.		
XX			
PA	(EOSB-) EOS BIOTECHNOLOGY INC.		
XX			
PI	Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;		
DR	WPI: 2002-471335/50.		
DR	N-PSDB: ABR92193.		
PT	Detecting a prostate cancer-associated transcript in a cell in a		
PT	patient, useful for diagnosing prostate cancer (PC) or screening		
PT	modulators of PC, by determining if prostate cancer-associated genes		
XX	are expressed in a prostate tissue		
PS	Claim 27; Page 363; 436pp; English.		
XX			
CC	The present invention relates to methods of detecting a prostate		
CC	cancer-associated transcript in a cell from a patient. The method		
CC	comprises contacting a biological sample from the patient with		
CC	prostate cancer-associated polynucleotides (designated PC genes) that		
CC	selectively hybridise to a sequence that is at least 80% identical		
CC	to them. The prostate cancer-associated polynucleotide sequences		
CC	are differentially expressed in prostate tumour tissue or in		
CC	prostate cancer and are derived from the tissues of various		
CC	organisms such as humans or other mammals (e.g. mice, sheep and dogs).		
CC	The methods of the invention are useful for diagnosing and creating		
CC	prostate cancer in mammals. The prostate cancer-associated genes are		
CC	useful for diagnosing or treating prostate cancer, as well as for		
CC	identifying modulators of prostate cancer or agents that inhibit		
CC	prostate cancer. The nucleic acid sequences are particularly useful		
CC	in gene therapy, as a vaccine or in antisense applications.		
CC	AB618100-AB619144 represent prostate cancer-associated proteins.		
XX			
SQ	Sequence 717 AA:		
QY	Query Match 22.6%; Score 730.5; DB 23; Length 717;		
Db	Best Local Similarity 36.9%; Pred. No. 9.3e-62;		
QY	Matches 182; Conservative 80; Mismatches 178; Indels 53; Gaps 10;		
QY	119 SFRCTDAEKNGGLILHYYSEREGLODIYIGIKTVAAQIHGTEIDMKYIOORNECDHTQ 178		
Db	187 SIICLDKE-DFELHYVYFFPRKRTSLILPGIIKAAHVLKTEHYVSLM-----PCCFHND 241		
QY	179 -----FLIEEKSEKEDFYEDLDRENGTOSRISPYT-FCKAFPHIIFDRD 226		
Db	242 CSEFVNQPYLLLYSHMKSTKPS-----LSPKPSQSLVPIPSLCKTPEPFHMFMDK 293		
QY	227 LVVYQGNALYRVLPQQLQPGNCSILVFSVLRPHIDISPHILSHINIVYFLVRSGEGLD 286		

Db 294 MTILPFGNGIRRLAMRDPQCKPNEFEIILTPKINQIFSGIMTMNQFVVRVRMDS 353
 QY 287 VEKLECEDELATGETEISCLAKCOMITLPEADSIILFCSPSVANLDDLTRRGHLYSDIPLH 346
 Db 354 VKK-----SSRVMDLKGOMIYVSSAILFLGSCVCRLEDFTRGILYSDIPLH 403
 QY 347 DATRLVLLGEOFRREYKLTQLELITDLRLQTLRALDEKKKTDPLLYSVLPVANEI. 406
 Db 404 NALRQVVLIGEQARADGLKRLKATLEQAHQALEEKKKTYDLLCSIFPCVEVAQL 463
 QY 407 RHKRPVPAKRDYNTILFSGIYGFNAFCSKHNSGEGAMIVLNDLYTRPTLDSRN 466
 Db 464 WOGVOVAKKFSNVTMLFSDIYGFALCSQCS----PIQVITMLNLYTRPQQCGELD- 518
 QY 467 PFVYVETVGDKYMTVSGILPEPCIHARSICHLALDMEIAGV-VOVDESVOITIGIT 525
 Db 519 --VYVETIAMPITVILGSLHKSQSDTHAVQIALMKMELSDVMSPHPEPIKMRIGLHS 576
 QY 526 GEVTVGVIGQMRPRICGNTVNLISRTETTGCKINSEYTYRCL-----MSP 575
 Db 577 GSVFAGVYGVKMPRCLEGNVTLANKEKSCSVPRKINVSPTYRLKDCPGFVFTPRSR 636
 QY 576 ENSDPOFHEHRG 588
 Db 637 EELPPNPFSEIRG 649

RESULT 8

ABB58042

ID ABB58042 standard; Protein; 676 AA.

XX ABB58042;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 918.

KW Drosophila: developmental biology; cell signalling; insecticide;
 pharmaceutical.

OS Drosophila melanogaster.

PN WO200171042-A2.

PD 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.

XX 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.

PI Venter JC, Adams M, Li PMD, Myers EW;

XX WPI, 2001-656660/75.

DR N-PSDB; ABL02145.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -

XX Disclosure: SEQ ID NO 918; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent

CC capable of detecting 1000 or more genes from Drosophila. The invention is

CC useful in developmental biology and in elucidating cell signalling and

CC cell-cell interactions in higher eukaryotes for the development of

CC insecticides, therapeutics and pharmaceutical drugs. The invention

CC discloses genomic DNA sequences (ABL16176-ABU30511), expressed DNA
 CC sequences (ABU01840-ABU16175) and the encoded proteins
 CC (ABU5737-ABU72072).

CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIP0

CC at ftp.wipo.int/pub/published_pot_sequences.

XX Query Match 22.5%; Score 726; DB 22; Length 676;

XX Best local Similarity 30.4%; Pred. No. 2.3e-61;

XX Matches 187; Conservative 125; Mismatches 235; Indels 68; Gaps 18;

SO Sequence 676 AA:

QY 22 MEDIRKKAOLDEGGQVLRIIYDDSKTYDLVAASVY-----NLNAGELIQFGKRFYF 77
 Db 73 WPIYTR-LKLDPO-----TRSCANYIYLDIQELIKMDASASEIILVYGEELITC 124
 QY 78 COESGYDITLRYLGSNVREFLONLDAHLHATITYGMRAPSEPCDARKGKLIHAYS 137
 Db 125 CCGTIERAFRCIGTDLGFLSGDGVYVLAKGEEDYDVTGVCA-----GEBELI-FTS 179
 QY 138 EREGLODIYIGITKVAQOIHGTEIDMKVYOORNE-----CDHTQ-FLIEEKES 186
 Db 180 ERVVIAMLLIGSLIKALTRMLYKVDVNIKIEPEGDARRYRLFSLVKDNSQFWMGRPTS 239
 QY 187 KEEDFYEDIDREENGTOESRISPYECKAPPHILFDDDLVYTOGGMATRYL-PQLP 245
 Db 240 VSKTIPETVQKSNSSNASDLOMNSSFCMFPWHFTMNOQLVQLGKPSKLYKPYMD 299
 QY 246 GNCSTLSVPSLVPRH-IDISFNGILSHINWVY--LRKRGILDYKLECEDELATGETIS 302
 Db 300 FGGQATTYDFDKRPKGLTKKFRDIYARITPFLIGLNNPGVANDPFAIG----- 348
 QY 303 CLRLKQOMITLPEADSIILFCSPSVANLDDLTRRGILYSDIPLHADRDLVLLGEOFR 362
 Db 349 -LEIKQOMVCHPESNSILFISPFILDLGICNGIFISDIPLDATREVIIVGEQARAQ 407
 QY 363 YKLTQELITDRLQTLRALDEKKKTDPLLYSVLPVYANBLRKRKRYPAKRYNVTI 422
 Db 408 DGLRRMDKIKNSIEPANSVATERKKNVSLRLFLPAPLAEKLMGSSIDAATYDVTI 467
 QY 423 LFSGIFNAFCSKHAEGAMKIVMLNDLYTRPFTLDSRNKP--YKYETVGDKYM 480
 Db 468 LFSDIYGFISCSRA--PFVYISMLGSLVKRDFEPD-----FFDYKNETIGDABC 518
 QY 481 TVSGLPKPCIHARSICHLALDMEIAGO-VOVDESVOITIGITGEVTVGVIGQMRP 539
 Db 519 VASGLIRASIIYDAHKVAMMALMKMIDACSKHITHDGRQIKMRIGLFTGYIAGVGRKMR 578
 QY 540 YCLFGNTVLTSTRTETTGCKINSEYTYRCLMSPENDPQFHEHRPVSMMKGRKPEM 599
 Db 579 YCLFGHSVTIANKFESGSEALKINVSPTTKDWLTKEHG--EPELQRPD-SFLPREP- 634
 QY 600 QWFLSRKNWGTET 614
 Db 635 -----NPGGTET 641

RESULT 9

ABB69903

ID ABB69903 standard; Protein; 669 AA.

XX ABB69903;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 36501.

KW Drosophila: developmental biology; cell signalling; insecticide;
 pharmaceutical.

OS Drosophila melanogaster.

PN WO200171042-A2.

XX 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US09231.
 XX 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX (PEKE) PE CORP NY.
 PA Venter JC, Adams M, Li PWD, Myers EW;
 XX WPI: 2001-656860/75.
 DR N-PSDB; ABL14006.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PS
 PS Disclosure; SEQ ID NO 36501; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
 CC sequences (AB101840-AB116175) and the encoded proteins
 CC (AB57737-AB572072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 XX Sequence 669 AA;
 SQ
 Query Match 21.8%; Score 704.5; DB 22; Length 669;
 Best Local Similarity 28.8%; Pred. No. 2.9e-59;
 Matches 197; Conservative 123; Mismatches 264; Indels 101; Gaps 18;
 QY 1 MYGCVNHALBELVIRNTPGEVMEDEKKEAQLDE--EGQFLVIRITYDDSKTDVLAASKV 58.
 DB 1 MYGMLYSEVOHYVQEEYGMETW--RKVCQIVCKHOSFKTHQIPKLPMPFAA--- 53
 QY 59 LNLNAGE-----ILQMFKMFVFCQESGYDTILRVLSNVREFQNLDAHDHATTPG 114
 DB 54 LSASTGSPFCQMFRCFCVRFNSNGYDKMIRSTGRFEDFQSIDNHVQKRYTPK 113
 QY 115 MRAPSECTDAEKKGILNHYSEREGLODIVIGITVAQIIGTEIDKVFIOQRNEEC 174
 DB 114 MKSPSQLTNMD-DDGAVIILYRSGRGTSKYLIGQMTEVAKEFYGLMTAVYLESQNDIC 172
 QY 175 DHQFLLEEKSEKEDPYEDLDRENGTQESRISPY-----TPCKAPFH 220
 DB 173 GGTAGPIKLTGEPITVYIKRDLDDNDYAKKRVNVAHPSQLKMPVDLNVLELPPFT 232
 QY 221 IIFDRDLVWQCGNAIYRVLPQLOPG-----NC----- 248
 DB 233 IVDHDKKITLAGKIVETWILNHPNPKTFIGSHILERKCKRRPDQIQOMETIILQMR 292
 QY 249 SLTSESLVR-----PHIDISFRT-----LSHINTVYLRSEGLDVERLEC-- 292
 DB 293 TVLFEFLIRTGHNRAAYDALNDFENFDEASSLNQAAMALASAEFSAEKKEEAAA 352
 QY 293 -----EDL-----ISCLRLKGOMIYLPEDASIIFLCPSVNWDDLRRLGYL 340
 DB 353 AATSKDIDPATGQRRHSVGRSTILKGMFYINDVSLFLCSPLENDLHIGIGLYL 412
 QY 341 SDIPLDADTVLLGQFREERYKLT-QELEIITRLQTLRALDEKKKTDTLLSYLP 399
 DB 413 NDLNPHGLSRELVWAGHOSKLEIMEKEQRSDLEKSLADSKRRQDDELTYMIP 472
 QY 400 PSVANEIRHKRPVPAKRYDNTIIFSGIVGFNAFCSKHASEGAMKTVNLINDLYTRPD 459
 DB 473 RPIAERMRKSEEHVQCSFEESVYFIETM--NIYDSGNNIQDAMQAVTTLNRY---FSA 527
 QY 460 LTDSRKRPFYKVTVDXKTYVSGLPKPCIHARSTICHLADMETAGOVYDGEVQI 519

DB 528 LDEEIISEFYKVTGVMAVYAGADVDNPLAEHACDLALRYMKRYKAHALPG--VAI 585
 QY 520 TIGHTGEVTVYGOMRPRYCLFGNTVNLSTRTTEGKGIKIVSEYTRCLMSPEND 579
 DB 586 RVGINSGVVAGVGMKPRICLFGDVTNARSRESSSDPMIOLSNY-----ALVQK 640
 QY 580 PQFHLERGPVSMKGRKEPMQWFL 604
 DB 641 VGYKVEARGFVKYKKGEMETWTL 665
 RESULT 10
 ABB69902
 ID ABB69902 standard; Protein; 649 AA.
 XX
 XX ABB69902;
 AC
 XX 26-MAR-2002 (first entry)
 DT
 XX Drosophila melanogaster polypeptide SEQ ID NO 36498.
 DE
 XX Drosophila: developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 KW Drosophila melanogaster.
 OS
 XX Drosophila melanogaster.
 XX
 XX WO200171042-A2.
 PD 27-SEP-2001.
 XX
 XX 23-MAR-2001; 2001WO-US09231.
 PF
 XX 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 XX (PEKE) PE CORP NY.
 PA Venter JC, Adams M, Li PWD, Myers EW;
 XX WPI: 2001-656860/75.
 DR N-PSDB; ABL14005.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PS
 PS Disclosure; SEQ ID NO 36498; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
 CC sequences (AB101840-AB116175) and the encoded proteins
 CC (AB57737-AB572072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 XX Sequence 649 AA;
 SQ
 Query Match 21.2%; Score 685; DB 22; Length 649;
 Best Local Similarity 28.5%; Pred. No. 2.2e-57;
 Matches 193; Conservative 122; Mismatches 256; Indels 106; Gaps 18;
 QY 1 MYGCVNHALBELVIRNTPGEVMEDEKKEAQLDEGQFLVIRITYDDSKTYDLVAASKV 60
 DB 1 MYGMLYSEVOHYVQEEYGMETW--RKVCQIVCKHOSFKTHQIPKLPMPFAA--- 53
 QY 61 LNLAGEIILQMGKMFVFCQESGYDTILRVLSNVREFQNLDAHDHATTPGMRAPSF 120

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Db DN-----FGYDKMIRSTGRYFCDFLOSIDNHLINRFTYPRKAKSPM 101
QY 121 RCTDAEKGGLLHAYSEREGLODIYIGIKTVAQOIHGTEDIMRVIOQRNECDHT--- 177
Db 102 QLTNMD-DNGAVIILYRSTRGSMKYLIGOMTEVAREFGLFKAVIYESQNDISGTAAP 160
QY 178 -----QTLIEKEKEKEDFYEDLRFENGQOERISYPT-----FCAAFPHILIFRD 226
Db 161 IKLDGPIPLTVKRYLDPDNREYMAKRVNTEAHPQOLKMPYKLDVFLDLFPFTFLVLMND 220
QY 227 LVTNOCGNATYRVLPLQDPG-----NC-----SLLSYF 254
Db 221 MKITHAGKIVETVIMHNPANPKSFIGHVNDLQCRRPKDTTIDMTLIMRAVLPEF 280
QY 255 SLVRP-HIDISFHTG-----LSHINTFVLRSKE---GLDVERKECEDEL- 296
Db 281 ELIRFGHNRRAAYDAVLNMDFENYDEMDLNEAQTALAKQERSESHPVDDDESARDEID 340
QY 297 --TGTE-----ISCRLKGOMTYLPEADSIILFCLSPSVANLDDLRRGILYLSIDIPLHAT 349
Db 341 PATGERRSSQGLRSTLLKGOMFYINDVSLIFLCSPLLEMLDELHGIGLYLNDLNPHGIS 400
QY 350 RDVLVLGEOFRREYKLT-QELEILTRLOLTLRALEDEKKTKDTLLYSVLPVANELRH 408
Db 401 RELVMAQMOHCKLEIMEKEKORDELEKSLADSKRODELLYSMPPIARML 460
QY 409 KRVPKARYDNVTILFSGIVGFNAFCSKHASEGAMKIVNLLNDLYTRFDLTLLSRKNPF 468
Db 461 SEEQCSQSFEEYSVIFLEVM--NVYDEGLNSIGAMQVNTLNKV---FSALDEELISPF 515
QY 469 YKVTYVGDKYTVTSGLPEPCIHARSICHLADMMELAGOVQV-DGESVOTTIGIHGE 527
Db 516 YKVTYVGMVYMAVSAGADVPNPLAEHACDLALRYMK---KRAHMDGVALARVGINSP 572
QY 528 VVTGIGIOMRPYCYLFGNTVNLTSRTETTGEGKINVSERYTCLMSPENSDPOFLEHR 587
Db 573 VVAGVVGOKVRPRYCYLFGDTVNTASRMSSSDPKIOLSKYT-----GDKVROYGYKVESR 627
QY 588 GPVSKKGKKEPMQVFL 604
Db 628 GTVQYKKGDMETWLL 644

RESULT 11
AA00754
ID AAG00754 standard; Protein; 119 AA.
XX
AC AAG00754;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein, SEQ ID NO: 4835.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-0200610.
XX
PR 26-FEB-1999; 99US-0122487.
XX
PA (GEST ) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR WPI; 2000-500381/45.
XX
DR N-PSDB; AAC00760.
XX

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PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
PS Claim 13; SEQ ID 4835; 71pp + CD-ROM; English.
XX
CC The present sequence is a polypeptide encoded by one of a large number
CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
CC were prepared from total human RNAs or polyA+ RNAs derived from 30
CC different tissues. EST sequences usually correspond mainly to the 3',
CC untranslated region (UTR) of the mRNA because they are often obtained
CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in
CC those cases where longer cDNA sequences have been obtained, the full 5'
CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
CC ends and can therefore be used to obtain full length cDNAs and genomic
CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
CC chromosome mapping procedures. They are used to obtain upstream
CC regulatory sequences and to design expression and secretion vectors.
SQ Sequence 119 AA:
QY Query Match 18.5%; Score 599; DB 21; Length 119;
Db Best Local Similarity 98.3%; Pred. No. 3.3e-50;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MGFVNAHELVIRNYGPEVWEDIKKEAQDDEGQFLYRIITDYSKTYDLVAASKVNLN 60
Db 1 MGFVNAHELVIRNYGPEVWEDIKKEAQDDEGQFLYRIITDYSKTYDLVAASKVNLN 60
QY 61 LNAGETLQFMGKMFYFCOESGYDTILRYLGSNVREFLONDLADHDLATYIPGMRAPS 119
Db 61 LNAGETLQFMGKMFYFCOESGYDTILRYLGSNVREFLONDLADHDLATYIPGMRAPS 119

RESULT 12
AA011280
ID AA011280 standard; Protein; 1061 AA.
XX
AC AA011280;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human atrionatriuretic peptide receptor A (NPR1) protein.
XX
KW Human; natriuretic peptide receptor A/guanylate cyclase A; NPR1;
KW atrionatriuretic peptide receptor A; haplotyping; cytostatic; genotyping;
KW haplotype pair; single nucleotide polymorphism; gene therapy;
KW drug screening; hypertension; hypotensive.
XX
OS Homo sapiens.
XX
PN WO200179231-A2.
XX
PD 25-OCT-2001.
XX
PF 16-APR-2001; 2001WO-0512300.
XX
PR 14-APR-2000; 2000US-197330P.
XX
PA (GENA-) GENA/ISSANCE PHARM INC.
XX
PI Bentivegna SC, Choi JY, Klem SE, Nandabalan K;
XX
DR WPI; 2002-066340/09.
XX
DR N-PSDB; AAS16995.
XX
PT Genotyping human natriuretic peptide receptor A/guanylate cyclase gene
PT of an individual, involves determining identity of nucleotide pair at
PT specific polymorphic sites for two copies of the gene
PS Claim 27; Fig 3; 96pp; English.
XX

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Sequence 1061 AA;

Query Match 14.9%; Score 481.5; DB 23; Length 1061;
 Best Local Similarity 27.7%; Pred. No. 3,6e-37;
 Matches 197; Conservative 88; Mismatches 227; Indels 199; Gaps 31;

33 EGGQFLVRIYDDSTKYDYLAASKVLN-----LNAGET 66
 416 ENGGRVAVLNNGT-SQELVAVSGRLNMPGYPEDIPKCGFEDNEDPACNODHSTLEV 474
 67 LQMFGRK-----FVFE-----COESGYDILRYLGSNVEFLQNALDHLATVTP 113
 475 LALVGSLSLGLIIVSFFIYRKQMLEKELASLWRYMREVDV-----SLERHL----- 524
 114 GNRAPSFCTDAEKK--GLIHYYSERBGLODIYIGIKTYAQOIHGTEDIMKTYOQBN 171
 525 --RSAGSRLLTSGRSGNSGSL-----TTGQFOY--FAKTAAYK--GMLVAVKRYNRKR 573
 172 EECDHOTPLIEKESKEEFYEDLDREFEENGTOESKISPT--FCAAFPHIIFDRLVVT 230
 574 IEL--TRKVFELKMRDQNHRLRFVAGCTDPNLCILTEYCPGSLQDILEMSITL 631
 231 -----QCGNATRYVLPOLPGN--CSLSVSLVRPHIDISFGILSHINTV---FVLR 279
 632 DMKRXSLNDIVKGMFLHNGAICS-----HGNLKSSNCVVDGFRVTK 675
 280 SKE-GILDVEKLECEDELGTETISCLRLKGOMIY--LPEADSTFLCSPSV--NMILD 333
 676 IDYGLSEFRDLDP-----QGHVYAKKLWTAPELLMAASPPVAGQAGDV 722
 334 TRRGILSDIP-----HATRD-----VLGEO--FREERYLQDELEL----- 372
 733 YSFGILDEIARSGVHEGIDLSPEKIEIERTNGEOPFRSIALQSHLELGLMOR 782
 373 -----TDRLQTLR-----ALEDKR 387
 783 CMAEDPQERPRQRIKRLKRNRENSNILDNLSRMOYANNLELYBERQATLEEK 842
 388 KKTDTLLYSVLPSPVANELRHRPPAKRYDNTLTLSGIVGFNAFCSKHASGEMKTY 447
 843 RRAEALTYOILPHSAEQLEKRETVQAEAFDSTVIYFSDIVGTALSAEST-----PMQV 898
 448 NLNLTYPEDTLTSRKNRPFYKVTYGDXYMTVSGLPKCH-----IARSLCHALDM 503
 899 TLNLDLYTCEDAVID---NEDYKVTETIDATNVVSGLP---VRNGLRACEPARALAL 952
 504 MEIAGOVQY---DGESVOITIGIHGEVNTYIGVGMPPRYCLFGANTVLTSTRTTEGKG 560
 953 LDVAVSFRIHRPQDLRLRIGIHGPVCAVGLKMPRYCLFGDVTNVASRMESNGEAL 1012
 561 KINSEYTYRCIMSPENDPQHLHRGVPYSMKKKEPMQVFLSKRNTGT 611
 1013 KIHLSSETKAVL-----EEFGFELKRGVEMKKGKVTYTWILGERGSST 1059

RESULT 14
 ABB11783
 ID ABB11783 standard; peptide; 1075 AA.
 XX
 AC ABB11783;
 XX
 DT 11-JAN-2002 (first entry)
 XX
 XX Human ANP-A receptor homologue, SEQ ID NO:2153.
 DE Human: cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KW inhibin; chemotaxis; chemokinesis; thrombolytic; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischaemia;
 KW bone disorder; osteoporosis; vascular growth disorder;

KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; antiinflammatory;
 KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
 KW cytosolic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
 KW antifungal; vulnereary; antilucer.
 XX
 OS Homo sapiens.
 XX
 PN WO200157188-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001WO-US03860.
 XX
 PR 03-FEB-2000; 2000US-0496914.
 PR 27-APR-2000; 2000US-0560875.
 XX
 PA (HYSR-) HYSR INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-457740/49.
 XX
 DR N-PSDB; ABA09027.
 XX
 PT Human proteins and DNA encoding sequences useful for preventing,
 PT treating or ameliorating a medical condition in a mammalian subject
 PT e.g. arthritis and cancer -
 PS
 XX
 PS Claim 20; Page 246-247; 1963pp; English.

Sequences ABB10981-ABB1230 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; haematopoiesis regulatory activity; tissue growth factor activity; immunomodulatory activity; activin- or inhibin-related activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis. depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human polypeptide of the invention.

Sequence 1075 AA;

Query Match 14.9%; Score 481.5; DB 22; Length 1075;
 Best Local Similarity 27.7%; Pred. No. 3,7e-37;
 Matches 197; Conservative 88; Mismatches 227; Indels 199; Gaps 31;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2003, 13:03:07 ; Search time 17.4966 Seconds
(without alignments)
3401.080 Million cell updates/sec

Title: US-09-762-767a-4
Sequence: 3231
1 MGFVNHALLLVIRNYGPE.....QVFLSRKNTGTEETKQDD 619

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR_73:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3231	100.0	619	1 S23097	guanylate cyclase
2	3206	99.2	619	1 OYB070	guanylate cyclase
3	3188	98.7	619	1 OYR01	guanylate cyclase
4	987	30.5	682	1 OYR02	guanylate cyclase
5	960.5	29.7	685	1 T1968	hypothetical prote
6	955	29.6	686	2 T23721	hypothetical prote
7	938	29.0	751	2 T24458	hypothetical prote
8	914	28.3	699	2 T18984	guanylate cyclase
9	909.5	28.1	732	2 S18325	guanylate cyclase
10	793	24.5	680	1 OYR01	guanylate cyclase
11	770	23.8	691	1 OYB07	guanylate cyclase
12	752.5	23.3	1099	2 T16822	hypothetical prote
13	730.5	22.6	717	2 S23098	guanylate cyclase
14	712	22.0	683	2 JH0810	guanylate cyclase
15	701.5	21.7	583	2 F88642	protein C5A4.3 [1
16	646.5	20.0	947	2 T20156	hypothetical prote
17	481.5	14.9	1061	1 OYH04	natriuretic peptid
18	470	14.5	1057	2 T15720	hypothetical prote
19	468	14.5	1057	1 OYR01	natriuretic peptid
20	466	14.5	1057	2 T15319	guanylate cyclase
21	466	14.4	1057	2 T57633	natriuretic peptid
22	457	14.1	1057	1 OYR01	natriuretic peptid
23	456.5	14.1	632	2 T31667	guanylate cyclase
24	455.5	14.1	632	2 T31666	natriuretic peptid
25	454.5	14.1	1047	1 OYR01	natriuretic peptid
26	453.5	14.0	1047	1 OYR01	natriuretic peptid
27	451	14.0	1525	1 A56699	guanylate cyclase
28	450.5	13.9	1047	2 T45882	guanylate cyclase
29	449.5	13.9	1025	2 T21319	hypothetical prote

30	443	13.7	1056	2 T33167	hypothetical prote
31	438.5	13.6	1110	1 S55279	guanylate cyclase
32	438.5	13.6	1112	2 T28082	hypothetical prote
33	431.5	13.4	1005	2 S33525	guanylate cyclase
34	429	13.3	1012	2 T24384	hypothetical prote
35	428.5	13.3	1018	2 A55915	guanylate cyclase
36	425	13.2	1050	2 S45636	natriuretic peptid
37	424	13.1	1068	2 T42382	guanylate cyclase
38	424	13.1	1108	2 T59385	guanylate cyclase
39	422	13.1	1102	2 JH0717	guanylate cyclase
40	420	13.0	1108	2 B55915	guanylate cyclase
41	419	13.0	1103	2 JC5581	guanylate cyclase
42	418	12.9	1122	2 T28130	hypothetical prote
43	416	12.9	1130	2 A89130	protein F52E1.4 [1
44	415.5	12.9	540	2 T34187	hypothetical prote
45	415.5	12.9	1110	2 I59370	guanylate cyclase

ALIGNMENTS

RESULT 1
S23097
guanylate cyclase (EC 4.6.1.2), soluble, 70k chain - human
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 20-Apr-2000
C:Accession: S23097
R:Guill, G.; Scholl, U.; Bulle, F.; Gueliaen, G.
FEBS Lett. 304, 83-88, 1992
A:Title: Molecular cloning of the cDNAs coding for the two subunits of soluble guanylate cyclase
A:Reference number: S23097; MIM:1352257; PMID:1352257
A:Accession: S23097
A:Molecule type: mRNA
A:Residues: 1-619 <GTD>
A:Cross-references: EMBL:X66533; NID:931685; PIDD:CAA4714.1; PID:931686
C:Genetics:
A:Gene: GDB:GUCY1B3; GUC1B3; GC-SB3
A:Cross-references: GDB:141992; OMIM:139397
A:Map position: 4q31.3-q33
C:Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic domain homology
C:Keywords: heterodimer; phosphorus-oxygen lyase
F:373-607/Domain: guanylate cyclase catalytic domain homology <GCC>

Query Match 100.0%; Score 3231; DB 1; Length 619;
Best Local Similarity 100.0%; Pred. No. 1.1e-215;
Matches 619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGFVNHALLLVIRNYGPEWEDIKKEAQLDEBGOFLVRIIYDSSKTYDLVAAASKVLN 60
DB	1	MGFVNHALLLVIRNYGPEWEDIKKEAQLDEBGOFLVRIIYDSSKTYDLVAAASKVLN 60
QY	61	LNNGEILOMFGKMFVYCOSSGYDTLIRVGSNNRELOLMDLHDLATITVGMRAPSF 120
DB	61	LNNGEILOMFGKMFVYCOSSGYDTLIRVGSNNRELOLMDLHDLATITVGMRAPSF 120
QY	121	RCTDAEKGKGLIHYYSERGLDIVIGITKTAQAQIHGETIDMKVYIQQNEBCHTOFL 180
DB	121	RCTDAEKGKGLIHYYSERGLDIVIGITKTAQAQIHGETIDMKVYIQQNEBCHTOFL 180
QY	181	IEEKESKEEDFYEDLDLFEENGTOESRISYTFCKAPPHIIPDRDLVYQCGNATYRVL 240
DB	181	IEEKESKEEDFYEDLDLFEENGTOESRISYTFCKAPPHIIPDRDLVYQCGNATYRVL 240
QY	241	POLQPGNCSTLVSFLVRPHIDISFGLSHINTVFLRSKEGLDVEKLECEDELTGTE 300
DB	241	POLQPGNCSTLVSFLVRPHIDISFGLSHINTVFLRSKEGLDVEKLECEDELTGTE 300
QY	301	ISCLRKGQMIYLPEDSILFLCSPVYNNLDDLIRGLYLSIDPLHADRDLVLLGQFR 360
DB	301	ISCLRKGQMIYLPEDSILFLCSPVYNNLDDLIRGLYLSIDPLHADRDLVLLGQFR 360
QY	361	EEKTLQDELTLDRDLTLRALDEKKKTDITLVSPLPSVANELHKKRPVPAKKRDNY 420
DB	361	EEKTLQDELTLDRDLTLRALDEKKKTDITLVSPLPSVANELHKKRPVPAKKRDNY 420

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Db      361 EEYKLTQLELITDRLOLTALAEDEKKRTDTLLYSVLPSPVANELRRKRPVPAKRYDNV 420
Qy      421 TILFSGIVGFNAFCSKHAASGEGAMKIYNLNDLYTRFDPTLDSRKNRPVYKVEYVGDKYM 480
Db      421 TILFSGIVGFNAFCSKHAASGEGAMKIYNLNDLYTRFDPTLDSRKNRPVYKVEYVGDKYM 480
Qy      481 TVSGIPEPCIHANSICHLADMEIAGOVVDGSEVOITIGIHTEGVVTVGIGORMPRY 540
Db      481 TVSGIPEPCIHANSICHLADMEIAGOVVDGSEVOITIGIHTEGVVTVGIGORMPRY 540
Qy      541 CLFGNTVVLTSRTETGTGKGINSEYTYRCLAMPENDPOPHLEHRGPVSMKGRKEPMQ 600
Db      541 CLFGNTVVLTSRTETGTGKGINSEYTYRCLAMPENDPOPHLEHRGPVSMKGRKEPMQ 600
Qy      601 VMFLSRKNTGTETRKODDD 619
Db      601 VMFLSRKNTGTETRKODDD 619

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RESULT 2

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OYR70
guanylate cyclase (EC 4.6.1.2), soluble, beta-1 chain - bovine
N:Alternate names: guanylate cyclase, soluble, 70k chain
C:Species: Bos primigenius taurus (cattle)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1999
C:Accession: S01653; A38759
R:Koesling, D.; Herz, J.; Gausepohl, H.; Nitromond, F.; Hlansch, K.D.; Boehm
FEBS Lett. 239, 29-34, 1988
A:Title: The primary structure of the 70 kDa subunit of bovine soluble guanylate cyclase
A:Reference number: S01653; MUID:89031214; PMID:2903071
A:Accession: S01653
A:Molecule type: mRNA
A:Residues: 1-619 <KOE>
A:Cross-references: EMBL:Y00770; NID:9407; PIDN:CMA68739.1; PID:9408
A:Accession: A38759
A:Molecule type: protein
A:Residues: 1-6; 28-32; 41-45; 96-109; 337-343; 396-406; 562-569 <KOE2>
C:Genetics:
A:Introns: 281/3; 392/2
C:Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic domain homology
C:Keywords: cGMP biosynthesis; heterodimer; phosphorus-oxygen lyase
F:373-607/Domain: guanylate cyclase catalytic domain homology <GCC>

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Query Match      99.2%; Score 3206; DB 1; Length 619;
Best Local Similarity 99.0%; Pred. No. 5.8e-214;
Matches 613; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MYGFVNHALLELVIRNTPGEVEMEDIKKEAQDDEGQFLVRIITYDSKTYDLVAASRYLN 60
Db      1 MYGFVNHALLELVIRNTPGEVEMEDIKKEAQDDEGQFLVRIITYDSKTYDLVAASRYLN 60
Qy      61 LNAGEIILQMFGRMFVFCQESGYDTILRVLSNVREFLQNDALHDHLATITPGMRAPSF 120
Db      61 LNAGEIILQMFGRMFVFCQESGYDTILRVLSNVREFLQNDALHDHLATITPGMRAPSF 120
Qy      121 RCTDAERKGLILHYSEREGLDIVIGITVAQOIHGTEIDMKVIOQRNECDHTQFL 180
Db      121 RCTDAERKGLILHYSEREGLDIVIGITVAQOIHGTEIDMKVIOQRNECDHTQFL 180
Qy      181 IEEKSEKEDFYEDLDREENGTOESRISPTPKAPFPHIIFRDVLYVQCGNAIYRVL 240
Db      181 IEEKSEKEDFYEDLDREENGTOESRISPTPKAPFPHIIFRDVLYVQCGNAIYRVL 240
Qy      241 POLQPGKCSLSVSLVRPHIDISFHGILSHINIVFLRSKGLLDVKECEDELGTGE 300
Db      241 POLQPGKCSLSVSLVRPHIDISFHGILSHINIVFLRSKGLLDVKECEDELGTGE 300
Qy      301 ISCLRKGOMIYLPDASSTILFCSPSVANNDDLRRLGLYLSIDIPLDHATRDVLLGEOFR 360
Db      301 ISCLRKGOMIYLPDASSTILFCSPSVANNDDLRRLGLYLSIDIPLDHATRDVLLGEOFR 360
Qy      361 EEYKLTQLELITDRLOLTALAEDEKKRTDTLLYSVLPSPVANELRRKRPVPAKRYDNV 420
Db      361 EEYKLTQLELITDRLOLTALAEDEKKRTDTLLYSVLPSPVANELRRKRPVPAKRYDNV 420

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Db      361 EEYKLTQLELITDRLOLTALAEDEKKRTDTLLYSVLPSPVANELRRKRPVPAKRYDNV 420
Qy      421 TILFSGIVGFNAFCSKHAASGEGAMKIYNLNDLYTRFDPTLDSRKNRPVYKVEYVGDKYM 480
Db      421 TILFSGIVGFNAFCSKHAASGEGAMKIYNLNDLYTRFDPTLDSRKNRPVYKVEYVGDKYM 480
Qy      481 TVSGIPEPCIHANSICHLADMEIAGOVVDGSEVOITIGIHTEGVVTVGIGORMPRY 540
Db      481 TVSGIPEPCIHANSICHLADMEIAGOVVDGSEVOITIGIHTEGVVTVGIGORMPRY 540
Qy      541 CLFGNTVVLTSRTETGTGKGINSEYTYRCLAMPENDPOPHLEHRGPVSMKGRKEPMQ 600
Db      541 CLFGNTVVLTSRTETGTGKGINSEYTYRCLAMPENDPOPHLEHRGPVSMKGRKEPMQ 600
Qy      601 VMFLSRKNTGTETRKODDD 619
Db      601 VMFLSRKNTGTETRKODDD 619

```

RESULT 3

```

OYR71
guanylate cyclase (EC 4.6.1.2), soluble, beta-1 chain - rat
N:Alternate names: guanylate cyclase, soluble, 70k chain
C:Species: Rattus norvegicus (Norway rat)
C>Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Jun-1999
C:Accession: A31871
R:Nakane, M.; Saheki, S.; Kuno, T.; Ishii, K.; Murad, F.
Biochem. Biophys. Res. Commun. 157, 1139-1147, 1988
A:Title: Molecular cloning of a cDNA coding for 70 kilodalton subunit of soluble guan
A:Reference number: A31871; MUID:89087429; PMID:2905128
A:Accession: A31871
A:Molecule type: mRNA
A:Residues: 1-619 <NAR>
A:Cross-references: GB:M22562; NID:9204273; PIDN:AAA41204.1; PID:9204274
C:Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic domain homology
C:Keywords: cGMP biosynthesis; heterodimer; phosphorus-oxygen lyase
F:373-607/Domain: guanylate cyclase catalytic domain homology <GCC>

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Query Match      98.7%; Score 3188; DB 1; Length 619;
Best Local Similarity 98.5%; Pred. No. 1e-212;
Matches 610; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy      1 MYGFVNHALLELVIRNTPGEVEMEDIKKEAQDDEGQFLVRIITYDSKTYDLVAASRYLN 60
Db      1 MYGFVNHALLELVIRNTPGEVEMEDIKKEAQDDEGQFLVRIITYDSKTYDLVAASRYLN 60
Qy      61 LNAGEIILQMFGRMFVFCQESGYDTILRVLSNVREFLQNDALHDHLATITPGMRAPSF 120
Db      61 LNAGEIILQMFGRMFVFCQESGYDTILRVLSNVREFLQNDALHDHLATITPGMRAPSF 120
Qy      121 RCTDAERKGLILHYSEREGLDIVIGITVAQOIHGTEIDMKVIOQRNECDHTQFL 180
Db      121 RCTDAERKGLILHYSEREGLDIVIGITVAQOIHGTEIDMKVIOQRNECDHTQFL 180
Qy      181 IEEKSEKEDFYEDLDREENGTOESRISPTPKAPFPHIIFRDVLYVQCGNAIYRVL 240
Db      181 IEEKSEKEDFYEDLDREENGTOESRISPTPKAPFPHIIFRDVLYVQCGNAIYRVL 240
Qy      241 POLQPGKCSLSVSLVRPHIDISFHGILSHINIVFLRSKGLLDVKECEDELGTGE 300
Db      241 POLQPGKCSLSVSLVRPHIDISFHGILSHINIVFLRSKGLLDVKECEDELGTGE 300
Qy      301 ISCLRKGOMIYLPDASSTILFCSPSVANNDDLRRLGLYLSIDIPLDHATRDVLLGEOFR 360
Db      301 ISCLRKGOMIYLPDASSTILFCSPSVANNDDLRRLGLYLSIDIPLDHATRDVLLGEOFR 360
Qy      361 EEYKLTQLELITDRLOLTALAEDEKKRTDTLLYSVLPSPVANELRRKRPVPAKRYDNV 420
Db      361 EEYKLTQLELITDRLOLTALAEDEKKRTDTLLYSVLPSPVANELRRKRPVPAKRYDNV 420
Qy      421 TILFSGIVGFNAFCSKHAASGEGAMKIYNLNDLYTRFDPTLDSRKNRPVYKVEYVGDKYM 480
Db      421 TILFSGIVGFNAFCSKHAASGEGAMKIYNLNDLYTRFDPTLDSRKNRPVYKVEYVGDKYM 480

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QY 481 TVSGIPEPCIHANSICHLALDMEIAGOVDSVOITIGIHGEVVTGVIQGRMPY 540
 DB 481 TVSGIPEPCIHANSICHLALDMEIAGOVDSVOITIGIHGEVVTGVIQGRMPY 540
 QY 541 CLFGVTVALTSRTETTGKRGKINSEYTYRCIMSPENDPOPHLEHRRGPVSKGKKEPMQ 600
 DB 541 CLFGVTVALTSRTETTGKRGKINSEYTYRCIMSPENDPOPHLEHRRGPVSKGKKEPMQ 600
 QY 601 VWFLSRKNTGTEETKODD 619
 DB 601 VWFLSRKNTGTEETKODD 619

RESULT 4

quanylate cyclase (EC-4.6.1.2), soluble, beta-2 chain - rat
 N:Alternat names: quanylate cyclase, soluble, 76k chain
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Jun-1999
 C:Accession: A36228
 R:Yuen, P.S.T.; Potter, L.R.; Garbers, D.L.
 Biochemistry 29, 10872-10878, 1990

A:Title: A new form of quanylyl cyclase is preferentially expressed in rat kidney.
 A:Reference number: A36228; MUID:91105012; PMID:1980215

A:Accession: A36228

A:Molecule type: mRNA

A:Residues: 1-682 <YUE>
 A:Cross-references: GB:M57507; GB:J05308; NID:9204279; PIDN:AAA41207.1; PID:9204280

A:Experimental source: kidney
 C:Superfamily: soluble quanylate cyclase; quanylate cyclase catalytic domain homology

C:Keywords: GMP biosynthesis, heterodimer, phosphorus-oxygen lyase

F:360-584/Domain: quanylate cyclase catalytic domain homology <GCC>

Query Match 30.5%; Score 987; DB 1; Length 682;
 Best Local Similarity 36.9%; Pred. No. 2.4e-60;

Matches 225; Conservative 104; Mismatches 195; Indels 86; Gaps 12;

QY 66 ILQMGKMFVFCQSGYDTILRVLSNVREFLQMLDLHDHATITPGMRAPSRCTDA 125
 DB 4 ILKLEGEYFFKCKSGYDRMLRTLGNLTERTEMLDLHSLALSTQEMNAPSRVEBG 63
 QY 126 EKGGLIAHYSEBGLDIIYIGIKTYAQQIHGEIDMKYIQQRNEC-----DHIOF 179
 DB 64 ADG-AMLHYSDRGLCHIVPGILTEAVAKDFPDVAMSLDM-NEEVERTGKEHYVF 121
 QY 180 LIEEKSEK-----EDFYED----- 194
 DB 122 LVQKAAHQIAGKAKSRQSGSDSOADBALOGTLIRMKERYLNIPVCPGKSHSTAVRA 181
 QY 195 -----LDREENGTOESRISPYTECKAPFHIIFEDRLVYTQCGNAIYRVLPOLP 245
 DB 182 SYLFEGKPLRDFQVYPERLMEVEEFCDAPEFHIVDEALRVQAAGNIOKYYPGILT 241
 QY 246 GNCSTLSFSLVRPHIDISFGILSHINTVYVLRSEKGLLDVEKLECEDELGTETISCLR 305
 DB 242 QKFALDEYFSIHPQVTNISSICKFINSOFLKTRKEMPRAR-----KSPQMLK 292
 QY 306 LKGOMIYLPDADSLIFLSPSYMNLDDLRLRGLYSDIPLHDATSDIVLLGQFBEYKL 365
 DB 293 LRGQITMESLROMCFMCSPNVRSLOLEESKMHLSIDLPADDTDLILNLOORLAEMEL 352
 QY 366 TOELEILDRLOTLRALEDEKKTDTLLSYLPSVANELLRHKRPVPAKRYDNTYIFS 425
 DB 353 SCQLEKKKEELRVLSNHLAIEKKETETLLYAMLPEHVANOQLEKGRVAAAGEETCTILFS 412
 QY 426 GIVGNAPCSKHAEGAMKYVNLINDLYTRPDTLDSKKNPYYKAVETVAGDKYTVSGL 485
 DB 413 DVVETFNIC---ACE-PIQIYMLNSMTSKEDRLTSVD---YKVEITIGDAYVYVGV 465
 QY 486 PEPCHHARSICHLALDMEIAGOV--VDGESVQITGSIHGEVVTGVIQGRMPYCLF 543
 DB 466 PVPESHQORVAFALGMRISAKEVNMPVTPGDIQIRGSIHGTAGVAGVADKMPRYCLF 525

QY 544 GNTVALTSRTETTGKRGKINSEYTYRCIMSPENDPOPHLEHRRGPVSKGKKEPMQ 603
 DB 526 GDTVATASMEHSHGLPSKYLHSLPTAHRAL-----KNGKEIYRROEIEYKGRK-MTYIF 579
 QY 604 LSRKNTGTE 613
 DB 580 LIQNLINATED 589

RESULT 5

hypothetical protein C46E1.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C:Accession: T19968; T23092

R:Lenhard, N.
 submitted to the EMBL Data Library, November 1997

A:Reference number: T19968

A:Accession: T19968

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-685 <WIL>

A:Cross-references: EMBL:AL008867; PIDN:CAA15512.1; GSPDB:GN00028; CESP:C46E1.2

A:Experimental source: clone C46E1

R:Lenhard, N.
 submitted to the EMBL Data Library, October 1997

A:Reference number: T19673

A:Accession: T23092

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-685 <WIL>

A:Cross-references: EMBL:299942; PIDN:CAB17073.1; GSPDB:GN00028; CESP:C46E1.2

A:Experimental source: clone H13M06

C:Genetics:

A:Gene: CESP:C46E1.2

A:Map position: X

A:Insertions: 11/3; 36/2; 70/1; 133/2; 179/1; 202/3; 258/2; 298/2; 301/3; 325/2; 405/2;

C:Superfamily: soluble quanylate cyclase; quanylate cyclase catalytic domain homology

Query Match 29.7%; Score 960.5; DB 2; Length 685;
 Best Local Similarity 34.2%; Pred. No. 1.6e-58;

Matches 220; Conservative 131; Mismatches 234; Indels 59; Gaps 17;

QY 2 YGFVNAHLALYIRNGPEWMDIRKEAOLDEGGLVRIYDDSKTYDLVAASVYLV 61
 DB 12 FGFHESIQIMIRYTGELFWSKVLERAGFEAGKENTIHNYISDADTESLVAASVYLV 71
 QY 62 NAGEILQMGKMFVFCQSGYDTILRVLSNVREFLQMLDLHDHATITPGMRAPSRCTDA 117
 DB 72 TREQVWEMYGCLIQYTMETGMDLIRSMKPLKGLNDLSLHYEIDHY--VYKANLNG 129
 QY 118 PSFRCIDAKGGLIAHYSEBGLDIIYIGIKTYAQQIHGEIDMKYIQQRNEC-----DHIOF 174
 DB 130 PSFRCIDAKGGLIAHYSEBGLDIIYIGIKTYAQQIHGEIDMKYIQQRNEC-----DHIOF 174
 QY 175 -----DHIOF-----EKESKEEDFYEDLDREENGTOESRISPYTECKAPFHIIF 225
 DB 189 TGERIEEYHIFVKTILNTQSNDEALGTVAVOHSNN--TKIRLTHADFISTPPIYAVYDQ 246
 QY 226 DLVATQCGNAIYRVLPQ--LQPGNSLLSVSLVRPHIDISFGILSHINTVYVLRSEKGL 284
 DB 247 DCKIYQVGBELYNHPRKDLISVGTPLMRIFEVTRPQIPDPDSICNFVAVVLYQVYTP 306
 QY 285 LDKER-----LECEDE-----LTGEISCLRKGMITYLPDADSLIFLSPSY 327
 DB 307 MEFORANRRAAOALAEASNLIEDNNGALALSOCHLKLKGMMLMSGCHIMTYLCSPPY 366
 QY 328 NMUDDITRGLYSDIPLDATRDVYLGEQFREFEYKQGELEITDRLOTLRALEDEK 387
 DB 367 TSIPELQGLKLTAMPPIHDPTDRLILQQRISDEVKMLQLEANNQJLENNAKDLLEVAK 426
 QY 388 KRTDITLVSVPSPVANELLRHKRPVPAKRYDNTYILFSGIYGFN--AFCSKHASGEGAM 444

Db 427 GKTDLALREMLPSPVAQOLKQGLSVEAREKEEATVMTDPTQOIVPLCT-----PK 479
 445 KIYNLNDLYTRDITLDSRKNPFYVYETVGDRTVSGLPBPCIHHSRICHALDM 504
 Db 480 DIHLNLELFTKDRGLGIC---AYKEVEVGSYSNMGVGIPLDYDHCYICHLAIGV 536
 Oy 505 ELAGOV--QVDSGVOITIGIHGEVVTGVIQGMPPRYCLFGNTVLTSTRTTGEKGI 562
 Db 537 MEKRYVDDPTTNPPLHFRAGISHGSPVAGVAGAMPYCCLEGDPTVNTSRMESHPIGRI 596
 Oy 563 NVEEYTRCLMSPENDPOFHLERHGPVSKGKKEPQWFLSR 606
 Db 597 HCEENAKKC-----AESTGRFEFEPGRGVQIKGGE-WNTYFLLR 635

RESULT 6

T23721

hypothetical protein M04G12.3 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000

C/Accession: T23721

R: Sims, M.

Submitted to the EMBL Data Library, October 1996

A/Reference number: Z19789

A/Accession: T23721

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-686 <MW1>

A/Cross-references: EMBL:281103; PIDN: CAB03210.1; GSPDB: GN00023; CESP: M04G12.3

A/Experimental source: clone M04G12

C/Genetics:

A/Gene: CESP: M04G12.3

A/Map position: 5

A/Intons: 1/3; 26/2; 60/1; 192/3; 255/2; 321/2; 401/2; 645/1

C/Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic domain homology

Query Match 29.68; Score 955; DB 2; Length 686;
 Best Local Similarity 34.28; Pred. No. 4e-58;

Matches 230; Conservative 126; Mismatches 235; Indels 82; Gaps 20;

Oy 1 MYGFVNHALLELVIRNYGPEWEDIKKEAQDEEGQFLVRIYIDSKTYDLVAASKRYLN 60
 1 MYGFVNHALLELVIRNYGPEWEDIKKEAQDEEGQFLVRIYIDSKTYDLVAASKRYLN 60
 Db 1 MFGFIHESINQVIRKYGEDYMLQVLERSGFENGKEIVNHYISDHYTVLVDSVSTVTK 60
 Oy 61 LNAGEILQMGKMFVFCOESGYDTILRVLSNVRELIQNDALH--DHLATY-PGMR 116
 61 LNAGEILQMGKMFVFCOESGYDTILRVLSNVRELIQNDALH--DHLATY-PGMR 116
 Db 61 VTRQDIWEMVGFLLTYSMELGMDLVRSKSPNKGFLMDLSLHYFIDHY--VYKANLR 118
 Oy 117 APSFRCDAEKGGILHYHYSEREGLODIYIGITVAQOIHGTEIDMKVYIQOINECD- 174
 117 APSFRCDAEKGGILHYHYSEREGLODIYIGITVAQOIHGTEIDMKVYIQOINECD- 174
 Db 119 GPSFRCEENPDGT-LMLHYFTGRPGLYHYGVAKVKEAKLVFMDISL-VVQGRTOHSV 176
 Oy 175 -----DHQFLIEKE-----SKEDFYEDLDPEENGTOESRISPY 211
 175 -----DHQFLIEKE-----SKEDFYEDLDPEENGTOESRISPY 211
 Db 177 MNGGERHEEVHIFILINKVEPRRDSSTISALTSVDPDGEIID-----DNKATSLQ 229
 Oy 212 TFCAPAPPHIIFRDLYVTCGNAYIRVLPQ--LQPGNCSLVSFLVRPHIDISFEGIL 269
 212 TFCAPAPPHIIFRDLYVTCGNAYIRVLPQ--LQPGNCSLVSFLVRPHIDISFEGIL 269
 Db 230 DFRALRYHFEVLDSCGLVQCGDELYNHPNELLOPQT-PILRIFEINRQIPLDPEINIC 288
 Oy 270 SHINTYFVLSKRGGL-----DVEKLECEDELGTETSC-LRKGQIVYL 313
 270 SHINTYFVLSKRGGL-----DVEKLECEDELGTETSC-LRKGQIVYL 313
 Db 289 NRTNNAFVLDVQKTSPLRKHKMANMATEKEEQEVAEVEEESNELTQGCILKKGQMMML 348
 Oy 314 PEADSLIFLCPSPVNMNDLTRGLYSLDIPLDATFADVLALGQFEEKEKTLQDEIELT 373
 314 PEADSLIFLCPSPVNMNDLTRGLYSLDIPLDATFADVLALGQFEEKEKTLQDEIELT 373
 Db 349 STKHIIYICSPVYISNELMORGMLTANPLADIRDLILLQORISDVENMLQLEANN 408
 Oy 374 DRLQTLRALDEKRRKTDLLYSVLPSPVANEDLRKRPVAKRYDNTYILFSGIVGNAP 433
 374 DRLQTLRALDEKRRKTDLLYSVLPSPVANEDLRKRPVAKRYDNTYILFSGIVGNAP 433
 Db 409 EOLETMTHELEVROKTDISILKMDLPRIAKKOLLGSHLEPCRYE-ATVAFCOLPAPFOI 467

Oy 434 ---CSKHASGEAMKIVNLNDLYTRDITLDSRKNPFYVYETVGDRTVSGLEPCT 490
 468 IPVCO-----PRNLIKLLNEVEFKDIRIVLRG--YKVEVSDSYVTGSDPYTS 517
 Db 491 HHARSICHLADMMELTAGOVQ--VDGESVOITIGIHGEVVTGVIQGMPPRYCLFGNTV 548
 491 HHARSICHLADMMELTAGOVQ--VDGESVOITIGIHGEVVTGVIQGMPPRYCLFGNTV 548
 Db 518 EHAENMCHVALGMMWEKRSYMDPVNKPPLLRIGLSGTITAGVGVGKMPRYCLFGEYTV 577
 Oy 549 LTRTETGEGKGINSEYTRCLMSPENDPOFHLERHGPVSKGKKEPQWFLSR-- 606
 549 LTRTETGEGKGINSEYTRCLMSPENDPOFHLERHGPVSKGKKEPQWFLSR-- 606
 Db 578 LASOMESLGVAGNIQCSSWY-----SKAMTGFEEPSPRKINVKRGD-VETYFLMRSL 632
 Oy 607 KNTGETEKODDD 619
 607 KNTGETEKODDD 619
 Db 633 KKSIMEITDHERD 645

RESULT 7

T24458

hypothetical protein T04D3.4 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000

C/Accession: T24458

R: Kershaw, J.

Submitted to the EMBL Data Library, October 1996

A/Reference number: Z19893

A/Accession: T24458

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-751 <MW1>

A/Cross-references: EMBL:281114; PIDN: CAB03288.1; GSPDB: GN00019; CESP: T04D3.4

A/Experimental source: clone T04D3

C/Genetics:

A/Gene: CESP: T04D3.4

A/Map position: 1

A/Intons: 1/3; 26/2; 95/3; 149/1; 213/3; 247/3; 291/3; 332/3; 369/2; 418/1; 462/3; 4

C/Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic domain homology

Query Match 29.04; Score 938; DB 2; Length 751;
 Best Local Similarity 35.04; Pred. No. 6.8e-57;

Matches 220; Conservative 125; Mismatches 236; Indels 48; Gaps 15;

Oy 1 MYGFVNHALLELVIRNYGPEWEDIKKEAQDEEGQFLVRIYIDSKTYDLVAASKRYLN 60
 1 MYGFVNHALLELVIRNYGPEWEDIKKEAQDEEGQFLVRIYIDSKTYDLVAASKRYLN 60
 Db 1 MFGMIHESFROLVTRKYGDIWEKIYHMSKFEIGTSEIENHYNDDETLVNSMANVIG 60
 Oy 61 LNAGEILQMGKMFVFCOESGYDTILRVLSNVRELIQNDALH--DHLATY-PGMR 116
 61 LNAGEILQMGKMFVFCOESGYDTILRVLSNVRELIQNDALH--DHLATY-PGMR 116
 Db 61 IPLEIWEAVGFLIOFTMETGMDLIRAMPDLGFLSDLSLHYFIDHY--VYTKLR 118
 Oy 117 APSFRCDAEKGGILHYHYSEREGLODIYIGITVAQOIHGTEIDMKVYIQOINECD- 175
 117 APSFRCDAEKGGILHYHYSEREGLODIYIGITVAQOIHGTEIDMKVYIQOINECD- 175
 Db 119 GPSFRCEENPDGT-LMLHYFTGRPGLYHYGVAKVKEAKLVFMDISL-VVQGRTOHSV 176
 Oy 176 -----HQPFLIEKE-----SKEDFYEDLDPEENGTOESRISPY 221
 176 -----HQPFLIEKE-----SKEDFYEDLDPEENGTOESRISPY 221
 Db 178 FTEHVAFFVLTQLENNASTQPKSISSKASQIDL---STGIYE--ISSDSFLAPYH 231
 Oy 222 IFRDLYVTCGNAYIRVLPQ--LQPGNCSLVSFLVRPHIDISFEGILHINTVFLYRSK 281
 222 IFRDLYVTCGNAYIRVLPQ--LQPGNCSLVSFLVRPHIDISFEGILHINTVFLYRSK 281
 Db 232 CFPDPLFVEHFGNFIRKTPFNAMROSTRVTDLELVHPEVPFESIKYKNSLAFPRK 291
 Oy 282 EGLDVEKLECEDELGTETSCRLKGQMYLPREADSILFLCSPVNMNDLTRGLYSLYS 341
 282 EGLDVEKLECEDELGTETSCRLKGQMYLPREADSILFLCSPVNMNDLTRGLYSLYS 341
 Db 292 -GLGDIY-----HNANDEAKTYLLKGSWFIIDEGRYIYMCSSVNTYVRELIERNHLS 344
 Oy 342 DIHLNATDVLVLSGQFREKYLQDELDLDRDLTLRALEDEKRRKTDLLYSVLPSS 401
 342 DIHLNATDVLVLSGQFREKYLQDELDLDRDLTLRALEDEKRRKTDLLYSVLPSS 401
 Db 345 DMQRHGTGTDVIMLNOSRMSQVELNRTLEETTKKLKMAQDEIEIKOKTDELCELPAS 404
 Oy 402 VANELRHKRPVPAKRDNTYILFSGIVGNAPSKASGAKMAYNLNDLYTRDITL 461
 402 VANELRHKRPVPAKRDNTYILFSGIVGNAPSKASGAKMAYNLNDLYTRDITL 461
 Db 405 VADSLSGRAMDAKFAADCTILFTDITVFTINCAKCTPYD---VTLNDLTLNRDRLV 460

QY 462 DSKNPFYKTYVGDKMTYVSGLEPCIHARSICHLALDMEIAGOV--QVDESVOI 519
 DB 461 GLHD---AYKETTIGDAMIYGVPERCENHAEFLNTISGIMLESKIVLSPITKPIKI 517
 QY 520 TIGITHTGVVGVIGORHPRYCLFGNTVNLSTRTTEGKINSEYTYRCLMSPEND 579
 DB 518 RLGHGCVGVAVGVGKIKPRYCLFGDITVNAVAKMESNIOCKIHAVE--TGKILGLAN 574
 QY 580 POFHLEHNGPVSMKGGKEPMQVWFLSRKN 608
 DB 575 PSYFIDRGNTEIRG-KGMATYFLERND 602

RESULT 8

T18984
 hypochelical protein C06B3.8 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
 C:Accession: T18984
 R:Pericy, C.
 submitted to the EMBL Data Library, July 1996
 A:Reference number: Z19056
 A:Accession: T18984
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-699 <MW>
 A:Cross-references: EMBL:Z77652; PIDN:CA01118.1; GSPDB:GN00023; CESP:C06B3.8
 A:Experimental source: clone C06B3
 C:Genetics:
 A:Gene: CESP:C06B3.8
 A:Map position: 5
 A:Introns: 1/3; 60/1; 192/3; 210/2; 270/2; 336/2; 415/2; 659/1
 C:Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic domain homology

Query Match 28.3% Score 914; DB 2: Length 699;
 Best Local Similarity 32.9% Pred. No. 2.8e-55;

Matches 219; Conservative 132; Mismatches 234; Indels 80; Gaps 19;

QY 1 MYGFVNAHLELVIRNYPREWEEDIKKEAOLDEGQFVRIYDSTKYDVAASKVLN 60
 DB 1 MFGFTHESIRQIVINYGEDWTQYVLESGFESGKENTMNYSDTIVLVDSVLYK 60
 QY 61 LNAGEIIOFGKMFVFCQESGYDTILRYLGSNVEFLONLDAH--DHATTY-PGMR 116
 DB 61 VTKDQVMEYGGELITTYSMELGMDLVSRMSPNLKFIDNLSLHYFIDH--VYKANLR 118
 QY 117 APSEFCTDAEKGKGLIHYISREGLDVIIGITVAQIHGTEIDMKVIOQRNEC-- 174
 DB 119 GPFSECEETPDGT-LLHYFTGRPLIYHVKGVAVKAVRPDLDTL--VVGRTQSVYH 176
 QY 175 -----DHQFLIEEKESKEDEYEDL-----DREENGTOES----- 206
 DB 177 MNGSRVEHEVYELINKKGGQFHPFLIAIVYSGSEPRNSESSEVSLSTNANPTIYD 236
 QY 207 ---RISPTTCKAFPHIIFBDRLVYTCGNATRYLPQ--IQPGNCSLVSFSLVRPHI 261
 DB 237 DTGLSLDQFSKALPYHEVYIDESCRLVOCSELAHNPIMELLQPGT-PILRFFEINRPOI 295
 QY 262 DISFGLISHINTVYVLSKESGLD-----VEKLECEDELSTETIS--CUL 306
 DB 296 PLDFENICGFINAVVLOYKTSPLKKKHAMDSOELEKQEMETLDEDAITNELAQGHHL 355
 QY 307 KGOMIYLRPADSILFLCSPSVNLDLIRGLYLSDIPLADATRDVLVLGPOFREBYKLT 366
 DB 366 KGOMMLASKKHIIYICSPYVTSINELMQGRITAMPPLHDAITRDILINQGRLSDEYVN 415
 QY 367 QDELEITRLQTLALDEKKKTDTLYSVLPSSVANELRKRPPAKRYNNVTILFSG 426
 DB 416 IQLENNQDLTMTRELEERQKTDSILKMLPRRLAQQLSGEHLAECEHE-ATVMPCD 474
 QY 427 IYGFNAF---CSKHASGEGAMKIYVNLNDLYTRPDTLDSRKKNPFYKTYVGDKMTYV 483

DB 475 LPAFOALPQCS-----PKDIYMLNEIFKKLDRIYVIRG---VYKVEYVSDSYMAVS 524
 QY 484 GLPEPCIHARSICHLALDMEIAGOV--QVDESVOITIGITHTGVVGVIGORHPRY 541
 DB 525 GIDPTPREAHNMCHVALGMMMEARSVIDPVSKTFLRLIGHSGITAGVGYVHPKVC 584
 QY 542 LFGNTVNLSTRTTEGKINSEYTYRCLMSPENDPOFHLHNGPVSMKGGKEPMQV 601
 DB 585 LFGETVTLASQMESISGMAGKIOCSKWAYOKAM-----ETGRFEFSPGRIDVR-QNGLTET 639
 QY 602 WFLSR 606
 DB 640 YFLTR 644

RESULT 9

S18325
 guanylate cyclase, soluble, alpha chain - human
 C:Species: *Homo sapiens* (man)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
 C:Accession: S18325
 R:Harteneck, C.; Medel, B.; Koesling, D.; Malkewitz, J.; Boehme, E.; Schultz, G.
 FEBS Lett. 292, 217-222, 1991
 A:Title: Molecular cloning and expression of a new alpha-subunit of soluble guanylyl
 A:Reference number: S18325; M0ID:92070494; PMID:1683630
 A:Accession: S18325
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-732 <HAB>
 A:Cross-references: EMBL:X63282; NID:g31670; PIDN:CAA44921.1; PID:g31671
 C:Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic domain homology
 F:473-701/Domain: guanylate cyclase catalytic domain homology <GCC>

Query Match 28.1% Score 909.5; DB 2: Length 732;
 Best Local Similarity 37.7% Pred. No. 6.1e-55;

Matches 208; Conservative 111; Mismatches 175; Indels 57; Gaps 14;

QY 51 LVAAASKVLNLNAGEIIOFGKMFVFCQESGYDTILRYLGSNVEFLONLDAHDLAT 110
 DB 154 ILQCVANILGLFEEIQRFGEEFNICFEN-ERYLRAVGGYLODFNGFALLEHINT 212
 QY 111 IY---PGMAPSEFCTDAEKGKGLIHYISREGLDVIIGITVAQIHGTEIDMKVY 167
 DB 213 SFGRQATLSPSPFLCKEPEGT-LMLHYHPHHIVGFAMGIMKAGKITY--RLDVEYE 269
 QY 168 QQRNE-----CDHTQFLIEEKESKEDEYEDLDLRFENGQESRISPYECKAF 217
 DB 270 QVANERKLCSDVSNPGNCSLTPLI--KECENTNIMKNLPQGSQVPADRLISINTFCRAF 327
 QY 218 PHIIIFDRDLVYTCGNATRYLPOLQPGNCSLSV-----FSLVRPHIDISFGLISH 271
 DB 328 PHLMDPMSVYLQAGEGLRKOL-----RCQTHKVLKFEDEFEIYSPVYNAFTFEVLLR 381
 QY 272 INTVYVLRKEGLIDVEKLECEDELTEGTE--ISCLRLKQMIYLRPADSILFLCSPSVN 329
 DB 382 LSTPEVIRK-----PEAGSSKNKQVMYKQMIHVPESNIIIFLFGPCVDK 429
 QY 330 LIDLFRGLYLSDIPLADATRDVLVLGPOFREBYKTOLEITDTLRLALDEBK 389
 DB 430 LDELMDRGHLHDIPRHDATRDVILVGEAKQDGLKRRMDIKALLETTHQALEBK 489
 QY 390 TDTLYSVLPSSVANELRKRPPAKRYNNVTILFSGIYGFNAFCSKHASGEGAMKIYVNL 449
 DB 490 TYDLYLSIRPGVYAOQLMOGOOQVAKRFEDVTMLFSDIYGFALICAOQ---PMQVISM 545
 QY 450 LNDLYTRPDTLDSRKKNPF--YKRYVYEDKMTYVSGLEPCIHARSICHLALDMEI 507
 DB 546 LNELYTRD-----HCCGLDITKYETIDATCAVAGLRKRSICAKKPTALMALKMEIS 600
 QY 508 IGVOV--DGSVOITIGITHTGVVGVIGORHPRYCLFGNTVNLSTRTTEGKINSE 566
 DB 601 EETLPDGRPIQMRIGIHSVSLAGVYVGRMPRYCLFGNNVTILASKEFSGSHRRINVP 660

QY	567	YTYRCIMSPEN	577
		:	:
Db	661	TTYQLKREES	671

RESULT 10

guanylate cyclase (EC 4.6.1.2), soluble, alpha-1 chain - rat
N:Alternate names: guanylate cyclase, soluble, 77k chain
C:Species: *Nattus norvegicus* (Norway rat)
C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Jun-1999
C:Accession: A38297
J:Nakane, M.; Arai, K.; Saheki, S.; Kuno, T.; Buechler, W.; Murad, F.
A:Title: Molecular cloning and expression of cDNAs coding for soluble guanylate cyclase
A:Reference number: A38297; PMID:1698769
A:Accession: A38297
A:Molecule type: mRNA
A:Residues: 1-690 <NNA>
A:Cross-references: GB:M57405; GB:M36075; NID:g204277; PIDN:AAA1206.1; PID:g204278
C:Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic domain homology
C:Keywords: cGMP biosynthesis; heterodimer; phosphorus-oxygen lyase
F:432-660/Domain: guanylate cyclase catalytic domain homology <GCC>

Query Match	24.5%	Score 793	DB 1	Length 690
Best Local Similarity	34.7%	Pred. No. 6.5e-47		
Matches 214	Conservative 100	Mismatches 215	Indels 88	Gaps 20

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0Y 27 KEAODIEGGEQVIRIITYDDSKTYEDVAAASKYLNINAGITLO-MFKGMEFYCOSGAYT 85
Db 102 KENNSSKEDLERIAEBA-----IAGVPY-----EVLKDSIGEELFKICYEDD-EH 149
QY 86 ILRVLGSVRELFONLMDL----HDILATYVPGMRAPSFCTDAEKGGILLHYSERE 140
Db 150 ILGVGGGLKPLNFSTLTKOSHCQBAERGRLEDAISILCLDKQ--DFLWVYFFPKR 208
QY 141 GLQDVIGIITVNAQIHGTEDMKVIOQ--RNEEDHQFL-----IEEKREDEDF 191
Db 209 TTAALLPGITIAAAILYESHVESLMPCCFSEB--TEFVQPYLLSVHVKSTKPS-- 264
QY 192 YEDLDREENGTOESRISPYT--FCKAPFPHIIFRDLVYVTOGMAIYRVLPOLO--PGNCS 249
Db 265 -----LSPGKQSSLVIPTSLECKTFPFHMLDBDLAILGNGIRLRVNRDPOGKPN 318
QY 250 LLSVFSVLVRPHIDISFHGILSHINTVFYLRKSKEGLLDYBKELECEDELGTETSLCRKQ 309
Db 319 FEEFFELTPKINQFSSIMTMLNQVILVRW-----DNLVKKSSRVADLKQ 368
QY 310 MIYLPKADSIIFLCSPSVWNLDDLTRRGILYSIDIPLEHADRDLVYLGEQFREERYKLTQEL 369
Db 369 MIYVESAILIFLGSPCVDRLEDFGRGLYLSDIPIHNAKRVLVIGEDARQODGLKRTL 428
QY 370 EILDRLQVLRALDEDEKKKTDTLLYSVLPBSVANELHRRKRPVPAKRYDNTVILFSGIYG 429
Db 429 GKLTATTEHAHQALEEKKKTVDDLCSIFPSEVAQOLWQGLVQAKKFNEYMTLPSDIYG 488
QY 430 FNARCSKRASEGAKKIYNLNDLTYTRRDTLTDSKNKFYVVEVYVGDKYMYVSGLEPBC 489
Db 489 FTAICSOQS----PLQVITMLNALYTRPDQOGEILD--YKVFETIGAYCVAGGILHRES 541
QY 490 IHHARSICHLADMEIEAGQV-QVDGESVQITIGIHTEGYVTVGVGQMRPRYCLFGNTVN 548
Db 542 DTHAVQIATMLAKMELSNENYMSPHGEPIKMRIGLHSSVFRAGVGVAKPRKICLGGNVT 601
QY 549 LTSRTETTGEGKINVSEYTYRCL-----MSPENDQF-----HL---EH 586
Db 602 LANFESCSVPRKINVSPTYRLLKDCGCVFTPRSRBELPBNFSPDIPGICHFLDAVOH 661
QY 587 RGPVSMCKKREPMQVWF 603
Db 662 QGPNS-----KPMF 670

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RESULT 11
OYB077

A:Residues: 1-691 <KOEL>
A:Cross-references: EMBL:X54014; NID:g405; PIDN:CAA37860.1; PID:g406
A:Accession: A38767
A:Molecule type: protein
A:Residues: 118-133; 226-232; 286-293; 319-330; 412-417; 557-571; 629-637 <KOE2>
C:Superfamily: Cys-loop guanylate cyclase; guanylate catalytic domain homology
C:Keywords: GMP biosynthesis; heterodimer; phosphorus-oxygen lyase
F:434-662/Domains: guanylate cyclase catalytic domain homology <GCC>

Query Match	23.8%;	Score 770;	DB 1;	length 691;
Best Local Similarity	33.9%;	Pred. No. 2.5e-45;		
Matches 205;	Conservative 90;	Mismatches 200;	Indels 110;	Gaps 16;

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QY 27 KEALDEGCVLWIIYDDSKTYDLVAASVILNLANGELL-QHFGMFVFCOESYDT 85
Db 104 KENKSILREDFEKTIVDQA-----IAGVV-----EIKESIGELFKRICYED-EX 151
QY 86 ILRVLSNVREELONLDALHDHLATYVPGMARPSFCTDAEKNG-----130
Db 152 ILGVVGGTLKPLNFSFSTL-----LKSSHCOAEK-KGREFASIIICLDKPD 199
QY 131 -LILHYYSEREGLDIYIGIIKTVAAQOIHGEIDMKVIAQORNECHDTQGLIEKESKEE 189
Db 200 VLYIYTFPPKITSILLPGIIKAARILITEVEVSSTPSR-----240
QY 190 DFEYEDLDRFENGTO-----ESRISPYT-FCKAPPHIIFRDLYV 229
Db 241 -FHODCEEVYDQPCELYSVHIRARSARPPPKPVSSLYVIPSALFCKTFPPHMDRUMSI 299
QY 230 TQGCNALIYRVLPQO-PGNCSLSVFSLVPHRPHDISHGILSHINTYFVLRSKGLDVE 288
Db 300 LQIHGIRLRILMSRDVQGKPPHDEYFELTPKISQTSQGTMTLMNMFVLVRW-----354
QY 289 KLECEDELGTGEISCLLKGOMIYLPADSIILFCSPSVMNLDLTPRGVLYSDIPLHDA 348
Db 355 -----DMSMKSSRYMDLKGOMIYMAVSSSITLFGSPCYORLEDFTRGLXISDIPRHNA 409
QY 349 TRDVLVIGEOFPREYKILTOELEIITDRLOTLRALDEKKKTDTLLVSVLPVANELRH 408
Db 410 LRDVLLVIGEOARADGGLTKRGLKATLEAOHAQALBEKKRKTYDLLCSIPSEVBARLWQ 469
QY 409 KRPPARKRYDNTILFSGIVGFNAFCRKHASGEAMKIYVNLNDLYRREPTLJDSRKNPF 468
Db 470 GHAQVARKFGVYVWLFSDIVGFTALCSQS-----PLAVITMLANLYRFRDQGEID-- 522
QY 469 VYKVEYVGDXYMYTSGLPBPCIHARISICHLALDMMELIAGO-VQVDEESQVITGITHGE 527
Db 523 VYKVEITIGDAVCVAGGLHKRESDFHAYQIALMALKMLMSHEVYVSPHEPIIKMRIGLHGS 582
QY 528 VYTGVIQORMPRYCLFSGNTVNLVSRTEGTGEKGINVSEYTYRCL-----MSPEN 577
Db 583 VFAGVYVVKMPRYCLFSGNTVNLANKFESGCVPRKINVSPTYRYLLKDCPGFVTFPRREE 642
QY 578 SDPQF 582
Db 643 LPNF 647

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RESULT 12
T16822

hypothetical protein T07D1.1 - Caenorhabditis elegans

C.Species: Caenorhabditis elegans

C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C.Accession: T16822

R.Leimback, D.

submitted to the EMBL Data Library, November 1995

A.Description: The sequence of C. elegans cosmid T07D1.

A.Reference number: Z18584

A.Accession: T16822

A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: DNA

A.Residues: 1-1099 <LEI>

A.Cross-references: EMBL:U04531; NID:g1109802; PID:g1109803; PIDN:AAA83158.1; CESP:T07D1

C.Genetics:

A.Gene: CESP:T07D1.1

A.Introns: 26/3; 94/3; 144/2; 200/3; 239/2; 278/3; 344/1; 382/2; 425/3; 474/3; 523/3; 61

Query Match 23.3%; Score 752.5; DB 2; Length 1099;

Best Local Similarity 29.9%; Pred. No. 86-44; Mismatches 254; Indels 117; Gaps 24;

Matches 211; Conservative 124; Mismatches 254; Indels 117; Gaps 24;

1 MYGFVNAHLELVINRGPEWEDIRKEAOLDEGQFLVRIYDSTKYDVAASKYLN 60

1 MYGLIDHIAIYIKKYESESTWSEVKFVSVYDD-TFQMDKKFSGLSHKLIMACHDVTG 59

61 LNAGEIILOMFGKMFVFCQESGYDT-----ILNVLGSNREPLQNDLHDHLLAT 110

60 DPVELMTNIGTSFKEFLTKFEFNKYVYLFIYIPVLANLGRTPQFLGNDLNEHYLAF 119

111 IYPGMARSPFCTDAEKKGILHYSSREGIADIVIGIKVAQOIHGTEIDMVIQ-Q 169

120 TFFPKLPSPFYC-EHESHTGLTHYRSKRGLHYVQOIRNISELQTEVAVIELDIE 178

170 RNECDHTQFLIEEKSEKEDFYEDLDFEENGTL-----QESRISPTFKAPFE 219

179 HDLNEHYIMRLH-----FNNLD-FNNGTAVRLNDSILEKVKITSDIFEDIRPF 228

220 HIIDRDILVYQCGNAITRYLPQLOPGNCSLSVSLVPRH-----DISF-- 265

229 IIVNRGRKIRNIGILRLVNAVIGY-GKKINQDTFLMRPFIRFMEVEYRGTRNYSFDI 286

266 -----HGILSHINTVPLVLS-----KRGILDVLELDEDELT 297

287 ACCDFRNFAPSKKRVKSVKSLHNSNITPELISDPIDHDEGIL-VYRTTVDQDT 345

298 -----GTETSLRLKGMITYLEADSLFLCSPSVANLDDLTRRGILYSLDIPDHAT 349

346 EERHMGDEGRKRLKFLSGOMFYMESWICFVGIPVSHLPQMKSGILFINDFALHSS 405

350 RDVLVLGQFREFRYLQLELILDR-LQITRLALEDEKKITDILLYSVLPVSANELRH 408

406 RDVLVASTQSAELKLLHQEAQSKRNKRNKRRRTDKLLQYMLPKPSVANQLRH 465

409 KRPAVA--KRYDNVITLFSGIYGFNAFCSKHAASGAKIYVLLNDLYTRFPLTDSRN 466

466 GESAVACCERDVSITLFTDIVEFPMKSSSLT-----PLEVIFELVITINFDKIITDYG- 520

467 PFVYKVFETVGDKMYVSGLEPCIHARSICHLADMEIAQV-QVYDGE--SVQITIGI 523

521 --VYKVFETIDAYVAVSGAPFTEHDAEFLIDCASQIYVEAGKVMNMNKKIKRIDRAGV 578

524 HTGEVYVAVIGQRMRYCLFGNTVNLSTRTTGKRGKINVESEYTRCLMSRNDP-QF 582

579 HSGSVAVAGVGLSMRYCLFGNTVYVANKMEONSSPMILVSETHNKKI---EESDPGLY 635

583 HLEHNGPYSMKGGKKEPMQVFL-----SRKNTGTEERKODD 618

636 QFERRELEIK-DDQTIOTFFVSRHGRVPSFPMNC---ESRQDD 677

C.Species: Homo sapiens (man)
C.Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C.Accession: S23098
R.Gjullu, G.; Scholl, U.; Bulle, F.; Guellaen, G.

FEBS Lett. 304, 83-88, 1992

A.Title: Molecular cloning of the cDNAs coding for the two subunits of soluble guanylyl

A.Reference number: S23097; MUID:92316204; PMID:1352257

A.Accession: S23098

A.Molecule type: mRNA

A.Residues: 1-717 <GII>

A.Cross-references: EMBL:X66534; NID:g31663; PIDN:CAA47145.1; PID:g31684

C.Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic domain homology

C.Keywords: heterodimer; phosphorus-oxygen lyase

F.430-658/Domain: guanylate cyclase catalytic domain homology <GCC>

Query Match 22.6%; Score 730.5; DB 2; Length 717;

Best Local Similarity 36.9%; Pred. No. 1.5e+42; Mismatches 182; Conservative 80; Mismatches 178; Indels 53; Gaps 10;

119 SFRCTDAKKGKGLILHYSSREGIADIVIGIKVAQOIHGTEIDMVIQOENRCDHTQ 178

187 SILCDKE-DDELHYTFPPKRTSLILPGIIKAAHVLVEVEVSLM---PCCFINDD 241

179 -----FLIEKSKEDFYEDLDFEENGTOSSRISPYT-FCKAPFRIIDRD 226

242 CSEFVNOPYLLSVNKKSTKPS-----LSPSKPSSLYLPSTLFCFTFFPHMFPKD 293

227 LVVTCGNATVYLPQLOPGNCSLSVSLVPRHIDISPHGILSHINTVYRSREGILLD 286

294 MIILOFGNGIRLNRKRFQGNPEYFEILPKINQTFSGIMTMNOMQVVRKMDNS 353

287 VEKLECEDELNGETEISCLRLKGMITYLEADSLFLCSPSVANLDDLTRRGILYSLDIPH 346

354 VKR-----SSRVMDLQGMITYVSSALIFLFGSCVDRLEDGFRGILYSLDIPH 403

347 DATRDVLVLGQFREFRYLQLELILDR-LQITRLALEDEKKITDILLYSVLPVSANEL 406

404 NALRDVVLIGEQRADQDGLKRLGKTLLEQAHOLEEKKKTYDLCISIPCEVAOL 463

407 RKRPRVPAKRYNTVITLFSGIYGFNAFCSKHAASGAKIYVLLNDLYTRFPLTDSRN 466

466 WQGVYVQAKKRSNTVMTLSIDYGFALCSQCS-----PLQVITMLNLTIRFQCCGEND 518

467 PFVYKVFETVGDKMYVSGLEPCIHARSICHLADMEIAQV-QVYDGEVQITIGIHT 525

519 --VYKVFETAMPITVILGILHRESPTHAVQIALMLKMEISDEVASPMGEPIKMLGLHS 576

526 GEVYVAVIGQRMRYCLFGNTVNLSTRTTGKRGKINVESEYTRCLMSRNDP-QF 582

577 GSVFAGVAVGKPRCLFGNTVNLANKRESQVPRKINVSPTTYRLKDCPGVFTPRSR 636

576 ENSDPQFHLHNG 588

637 EELPPNFSEIRP 649

RESULT 14

JH0810

guanylate cyclase (EC 4.6.1.2) - fruit fly (Drosophila melanogaster)

C.Species: Drosophila melanogaster

C.Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 26-Aug-1999

C.Accession: JH0810

R.Yoshikawa, S.; Miyamoto, I.; Aruga, J.; Furutachi, T.; Okano, H.; Mikoshiba, K.

J. Neurochem. 60, 1570-1573, 1993

A.Title: Isolation of a Drosophila gene encoding a head-specific guanylyl cyclase.

A.Reference number: JH0810; MUID:93203896; PMID:809578

A.Accession: JH0810

A.Molecule type: mRNA

A.Residues: 1-683 <YOS>

A.Cross-references: GB:S57126; NID:g298674; PID:g298675

A.Experimental source: head

A.Gene: dgc 1

RESULT 13
S23098
guanylate cyclase (EC 4.6.1.2), soluble, 81k chain - human

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 27, 2003, 12:55:07 ; Search time 11.0695 Seconds

(without alignments)
2585.358 Million cell updates/sec

Title: US-09-762-767a-2

Perfect score: 3593

Sequence: 1 MFCYKLDKLTGECPSLL.....OKDVEDGNANFLKASGID 690

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	3593	100.0	690	1	CYG3_HUMAN
2	3323	90.0	690	1	CYG3_RAT
3	3107.5	86.5	691	1	CYG3_BOVIN
4	1651	46.0	730	1	CYG4_RAT
5	1635	45.5	732	1	CYG4_HUMAN
6	976.5	27.2	683	1	CYGH_DROME
7	795	22.1	619	1	CYG1_RAT
8	793.5	22.1	619	1	CYG1_BOVIN
9	789.5	22.0	619	1	CYG1_HUMAN
10	774.5	21.6	682	1	CYG2_RAT
11	708	19.7	617	1	CYG2_HUMAN
12	460	12.8	1047	1	ANPB_BOVIN
13	460	12.8	1047	1	ANPB_HUMAN
14	460	12.8	1047	1	ANPB_RAT
15	457.5	12.7	1057	1	ANPB_RAT
16	456.5	12.7	1061	1	ANPB_HUMAN
17	454.5	12.6	1057	1	ANPB_MOUSE
18	452	12.6	433	1	KSCG_RAT
19	450	12.5	1108	1	CYGE_MOUSE
20	448	12.5	1108	1	CYGE_RAT
21	445	12.4	1109	1	CYGD_CANFA
22	442	12.3	1108	1	CYGF_HUMAN
23	440	12.2	1103	1	CYGF_BOVIN
24	438	12.2	1110	1	CYGF_RAT
25	438	12.2	1110	1	CYGD_BOVIN
26	434	12.1	1103	1	CYGD_HUMAN
27	430	12.0	1110	1	CYGE_RAT
28	428.5	11.9	1050	1	ANPB_RAT
29	427	11.9	1125	1	CYGS_STRPU
30	414.5	11.5	1073	1	HSER_PIG
31	408.5	11.4	1073	1	HSER_HUMAN
32	407.5	11.3	1072	1	HSER_RAT
33	399.5	11.1	1076	1	HSER_CAVPO

34	389	10.8	1137	1	CYG1_CAEBL	Q09435 caenorhabdi
35	322.5	9.0	887	1	CYA2_HUMAN	Q08462 homo sapien
36	322	9.0	1064	1	CYA2_RAT	P26770 rattus norv
37	319.5	8.9	1099	1	CYA7_MOUSE	P51829 mus musculu
38	319	8.9	1090	1	CYA2_RAT	P26769 rattus norv
39	316	8.8	1080	1	CYA7_HUMAN	P51828 homo sapien
40	310.5	8.6	1078	1	CYA7_BOVIN	Q28450 bos taurus
41	303.5	8.4	1144	1	CYA3_HUMAN	O60266 homo sapien
42	303	8.4	1144	1	CYA3_RAT	P21932 rattus norv
43	302	8.4	1134	1	CYAL_BOVIN	P19754 bos taurus
44	290.5	8.1	2248	1	CYAL_DROME	P32870 drosophila
45	287.5	8.0	1249	1	CYA8_MOUSE	P97490 mus musculu

ALIGNMENTS

RESULT 1
ID CYG3_HUMAN STANDARD; PRT; 690 AA.
AC Q02108; O43843;
DT 01-JUL-1993 (Rel. 26, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Guanylate cyclase soluble, alpha-1 chain (EC 4.6.1.2) (GCS-alpha-1)
DE (Soluble guanylate cyclase large subunit) (GCS-alpha-3).
GN GUCY1A1 OR GUCY1A3 OR GUC1A3 OR GUCSA3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92316204; PubMed=1352257;
RA Giullit G., Scholl U., Bulle F., Guejlaen G.;
RT Molecular cloning of the cDNAs coding for the two subunits of
RT soluble guanylyl cyclase from human brain.";
RL FEBS Lett. 304:83-88(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Ganssemans Y., Brockaert P., Fiers W.;
RT "Human soluble guanylate cyclase large subunit mRNA, alpha3-like.";
RL Submitted (MAY-1996) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98416113; PubMed=9742212;
RA Zabel U., Weeger M., La M., Schmidt H.H.;
RT "Human soluble guanylate cyclase: functional expression and revised
RT isoenzyme family.";
RL Biochem. J. 335:51-57(1998).
CC -I- CATALYTIC ACTIVITY: GTP -> 3',5'-cyclic GMP + diphosphate.
CC -I- ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE OF
CC MAGNESIUM OR MANGANESE IONS.
CC -I- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
CC -I- MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES: SOLUBLE
CC FORMS AND MEMBRANE ASSOCIATED RECEPTOR FORMS.
CC -I- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
CC FAMILY.
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CC or send an email to license@isb-sb.ch).
CC -----
CC EMBL: X66534; CAA47145.1; -;
CC EMBL: U58855; AAB94794.1; -;

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DR EMBL: Y15723; CAA75738.1; -.
DR PIR: S23098; S23098.
DR HSSP: P19687; 1AMN.
DR Genew: HGNC:4685; GUCY1A3.
DR MIM: 139396; -.
DR InterPro: IPR001054; G_cyclase.
DR Pfam: PF00211; guanylate_cyc; 1.
DR SMART: SM00044; CYCC; 1.
DR PROSITE: PS00452; GUANYLATE_CYCLASES_1; 1.
DR PROSITE: PS00125; GUANYLATE_CYCLASES_2; 1.
DR Lysase: CGMP synthesis: Multigene family.
KM DOMAIN 481 608 GUANYLATE_CYCLASE.
FT CONFLICT 124 127 AAG -> QQS (IN REF. 1).
FT CONFLICT 131 184 VIKESIGEVEFKICEEDENILGVGGTLDPLNFSSTLLK
LEAPLKIFKOLQYPTSETEQPLRSRKKQ (IN REF.
1).
FT CONFLICT 322 322 MISSING (IN REF. 1).
FT CONFLICT 529 535 GDAICVA -> AMPTVWL (IN REF. 1).
FT CONFLICT 678 690 GNAFNLKASGID -> ASQFPRQISNRRLATYPIYKSLG
FDSLKMCRASESTIGIDG (IN REF. 1).
SQ SEQUENCE 690 AA; 77452 MW; DAIEI4ASEI145ICF CRC64;
Query Match 100.0%; Score 3593; DB 1; Length 690;
Best Local Similarity 100.0%; Pred. No. 2.7e-243;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFCSTKLKDKITGECFSLILAPGQVNPSESEEAAGSSSEKATVPICODIPEKNIOESLP 60
DB 1 MFCSTKLKDKITGECFSLILAPGQVNPSESEEAAGSSSEKATVPICODIPEKNIOESLP 60
QY 61 QRTSRSRYVLHTLAESICKLIPPEERLNVALLQRTLAKHKIKESKSLERDEFKTI 120
DB 61 QRTSRSRYVLHTLAESICKLIPPEERLNVALLQRTLAKHKIKESKSLERDEFKTI 120
QY 121 QAAAGAPVAVIKESIGEVEFKICEEDENILGVGGTLDPLNFSSTLLKOSHCQ 180
DB 121 QAAAGAPVAVIKESIGEVEFKICEEDENILGVGGTLDPLNFSSTLLKOSHCQ 180
QY 181 KRGRLDASILCLDKEDDFLHVVYFPPKRTSLIPGIIKAAHVLTEVEVSLMP 240
DB 181 KRGRLDASILCLDKEDDFLHVVYFPPKRTSLIPGIIKAAHVLTEVEVSLMP 240
QY 241 HNCSEVNPYLLSYHMAKSTPSLSPKPOSSLVPTSLFCTPFPHMFDMKMTILQ 300
DB 241 HNCSEVNPYLLSYHMAKSTPSLSPKPOSSLVPTSLFCTPFPHMFDMKMTILQ 300
QY 301 FNGSIRRLMRDPFOGKPNFEVEFEILTPIKINOTFGSITMLNMQFVVRVRMDNSYK 360
DB 301 FNGSIRRLMRDPFOGKPNFEVEFEILTPIKINOTFGSITMLNMQFVVRVRMDNSYK 360
QY 361 SRVMDLKGOMIYVSSAILFLGSPCVRLDEFTGRGLYLSIDIPINHALRDVYLIG 420
DB 361 SRVMDLKGOMIYVSSAILFLGSPCVRLDEFTGRGLYLSIDIPINHALRDVYLIG 420
QY 421 AOGGLKRRGLKRLATLEQAQALAEKKKTVDDLCSIFPEVAQOLMQGVQAKKSNV 480
DB 421 AOGGLKRRGLKRLATLEQAQALAEKKKTVDDLCSIFPEVAQOLMQGVQAKKSNV 480
QY 481 TMLFSDIVGFTALCSQSPLOVITMLNALTREDOCGEIDYKVEITIGAYCYAGSL 540
DB 481 TMLFSDIVGFTALCSQSPLOVITMLNALTREDOCGEIDYKVEITIGAYCYAGSL 540
QY 541 ESDTHAVQALMALKMEISDEVMSPHGEDIKMRIGLHSGSVTAVGVVGMKPRYCL 600
DB 541 ESDTHAVQALMALKMEISDEVMSPHGEDIKMRIGLHSGSVTAVGVVGMKPRYCL 600
QY 601 VTLANKFESGVRKINVSPTTYRLKDCGPFVTPSRSELPNPFSEIPGICHTDAY 660
DB 601 VTLANKFESGVRKINVSPTTYRLKDCGPFVTPSRSELPNPFSEIPGICHTDAY 660
QY 661 QOGTNSKPCFOKKDVEDGNANFLGKASGID 690
DB 661 QOGTNSKPCFOKKDVEDGNANFLGKASGID 690

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DB 661 QOGTNSKPCFOKKDVEDGNANFLGKASGID 690
RESULT 2
CYG3_RAT
ID CYG3_RAT STANDARD; PRT; 690 AA.
AC P19686;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Guanylate cyclase soluble, alpha-1 chain (EC 4.6.1.2) (GCS-alpha-1)
DE (soluble guanylate cyclase large subunit).
GN GUCY1A1 OR GUCY1A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID-10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE-Lung;
RX MEDLINE-91009100; Pubmed-1698769;
RA Nakane M., Arai K., Sahel S., Kuno T., Buechler W., Murad F.;
RT "Molecular cloning and expression of cDNAs coding for soluble
guanylate cyclase from rat lung.";
RL J. Biol. Chem. 265:16841-16845(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley; TISSUE-Striatum;
RX MEDLINE-97151525; Pubmed-8997507;
RA Smigrodzki R.M., Levitt P.;
RT "The alpha 1 subunit of soluble guanylyl cyclase is expressed
prenatally in the rat brain.";
RL Brain Res. Dev. Brain Res. 97:226-234(1996).
CC -1- CATALYTIC ACTIVITY: GTP -> 3',5'-cyclic GMP + diphosphate.
CC -1- ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE OF
MAGNESIUM OR MANGANESE IONS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES: SOLUBLE
FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
CC -1- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
FAMILY.
CC
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CC -----
DR EMBL: M57405; AAA41206.1; -.
DR PIR: A38297; OYRTAL.
DR HSSP: P19687; 1AMN.
DR InterPro: IPR001054; G_cyclase.
DR Pfam: PF00211; guanylate_cyc; 1.
DR SMART: SM00044; CYCC; 1.
DR PROSITE: PS00452; GUANYLATE_CYCLASES_1; 1.
DR PROSITE: PS00125; GUANYLATE_CYCLASES_2; 1.
KM Lysase: CGMP synthesis: Multigene family.
FT DOMAIN 480 607 GUANYLATE_CYCLASE.
SQ SEQUENCE 690 AA; 77566 MW; E4819B2CA4F86401 CRC64;
Query Match 90.0%; Score 3232; DB 1; Length 690;
Best Local Similarity 89.1%; Pred. No. 4.3e-218;
Matches 616; Conservative 39; Mismatches 34; Indels 2; Gaps 2;
QY 1 MFCSTKLKDKITGECFSLILAPGQVNPSESEEAAGSSSEKATVPICODIPEKNIOESLP 60
DB 1 MFCSTKLKDKITGECFSLILAPGQVNPSESEEAAGSSSEKATVPICODIPEKNIOESLP 60
QY 61 QRTSRSRYVLHTLAESICKLIPPEERLNVALLQRTLAKHKIKESKSLERDEFKTI 120
DB 61 QRTSRSRYVLHTLAESICKLIPPEERLNVALLQRTLAKHKIKESKSLERDEFKTI 120

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Db      60 QKRTSKRNYLHTLHESIKLTPFERERLNLQRLTAHKKIKENNSSKEDELETLAE 119
QY      121 QAAVAGVPVEVNIKESIGEVEFKICYEDENIIGVGGTLKDFLNSFTLLKQSSHCQEA 180
      120 EAIAGVPEVNIKESIGEELFKICYEDEHIIIGVGGTLKDFLNSFTLLKQSSHCQEA 179
QY      181 KGRLEDASILLCKEDDFLHYFFPPKRTTSLILPGIITKAAHVLETEVEVSLMPPCF 240
      180 RGRLEDASILLCKEDDFLHYFFPPKRTTSLILPGIITKAAHVLETEVEVSLMPPCF 239
QY      241 HNDCEFEVNOPYLTVSVHMKSTPSPKPOSSLVPTSLCKTPEFHMDKMTILQ 300
      240 RSCCEFEVNOPYLTVSVHMKSTPSPKPOSSLVPTSLCKTPEFHMDKMTILQ 299
QY      301 FCGNGIRLNNRRDFOGKPNFEFEFLITPKINOTFGSITMLNMQFVVRVRMDNSVKKS 360
      300 LCGNGIRLNNRRDFOGKPNFEFEFLITPKINOTFGSITMLNMQFVVRVRMDNSVKKS 359
QY      361 SRVMDLKGOMIYVSSAILFLGSPCVDRLEDFTGRLGLYLSDIPIHNLADVVLIGEQA 420
      360 SRVMDLKGOMIYVSSAILFLGSPCVDRLEDFTGRLGLYLSDIPIHNLADVVLIGEQA 419
QY      421 ADDGLKRRIGKTKATEAOHQAOLEEKKKTVDLLCSIFCEVAQOIMOGVQAKKESNV 480
      420 ADDGLKRRIGKTKATEAOHQAOLEEKKKTVDLLCSIFCEVAQOIMOGVQAKKESNV 479
QY      481 TMLFSDIVGFTALICSCSPLOVITMLNALTFRDQCGELDYKVTETIGAYCVAGGLH 540
      480 TMLFSDIVGFTALICSCSPLOVITMLNALTFRDQCGELDYKVTETIGAYCVAGGLH 539
QY      541 ESDTHAVQIALMALKMMELSDDEVSPHGEPIKMRIGLHSGSVAGVGVKMPRYCLGNN 600
      540 ESDTHAVQIALMALKMMELSDDEVSPHGEPIKMRIGLHSGSVAGVGVKMPRYCLGNN 599
QY      601 VTLANFESCSVPKRTINVSPTTYRLKDCGFYFPRSRRELPNPESEIPGICHTLDAY 660
      600 VTLANFESCSVPKRTINVSPTTYRLKDCGFYFPRSRRELPNPESEIPGICHTLDAY 659
QY      661 Q-OGTNSKPCFOKKEDVGNANFLGRASGID 690
      660 QHGGPNSKPMFOQKDAEDGNANFLGRASGID 690
Db

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RESULT 3

CY33_BOVIN

ID CY33_BOVIN STANDARD; PRT; 691 AA.

AC P19687;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Guanylate cyclase soluble, alpha-1 chain (EC 4.6.1.2) (GCS-alpha-1)

DE (Soluble guanylate cyclase large subunit).

GN GUCYAL1 OR GUCYAL1.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_Taxid=9913;

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE=Adrenal medulla;

RX MEDLINE=90306336; PubMed=1973124;

RA Koesling D., Harteneck C., Humbert P., Bosserhoff A., Frank R.,

RA Schultz G., Boehme E.;

RT "The primary structure of the larger subunit of soluble guanylyl

RT cyclase from bovine lung. Homology between the two subunits of the

RT enzyme.";

RL FEBS Lett. 266:128-132(1990).

RN [2].

RX 3D-STRUCTURE MODELING OF 472-628.

RX MEDLINE=98054247; PubMed=9391039;

RA Liu Y., Ruoho A.E., Rao V.D., Hurley J.H.;

```

RT      "Catalytic mechanism of the adenylyl and guanylyl cyclases: modeling
RT      and mutational analysis.";
RL      Proc. Natl. Acad. Sci. U.S.A. 94:13414-13419(1997).
CC      -1- CATALYTIC ACTIVITY: GTP -> 3',5'-cyclic GMP + diphosphate.
CC      -1- ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE OF
CC      MAGNESIUM OR MANGANESE IONS.
CC      -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC      -1- MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES: SOLUBLE
CC      FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
CC      -1- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
CC      FAMILY.
CC      -----
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CC      between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; X54014; CAA37960.1; -.
DR      PIR; S10713; OYB077.
DR      PDB; 1AMN; 28-JAN-98.
DR      InterPro; IPR001054; G_cyclase.
DR      Pfam; PF00211; guanylate_cyc; 1.
DR      SMART; SM00044; CYCC; 1.
DR      PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.
DR      PROSITE; PS00125; GUANYLATE_CYCLASES_2; 1.
DR      K1; LYase; GMP synthetase; Multigene family; 3D-structure.
FT      DOMAIN
FT      SQUENCE 691 AA; 77532 MW; 5D1FE4D2204E8683 CRC64;

```

Query Match 86.5%; Score 3107.5; DB 1; Length 691;

Best Local Similarity 86.1%; Pred. No. 2,1e-209;

Matches 595; Conservative 41; Mismatches 54; Indels 1; Gaps 1;

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QY      1 MFCYTKLKDITGECPSLAPGVNPSESEAGSSESCATVP-ICODIPKNTQESTL 59
      1 MFCYTKLKDITGDCPSLAPGVNPSESEAGSSESCATVPQGVCPVPKPNPGRLL 60
Db
QY      60 POKRTSKRYLHTLHESIKLTPFERERLNLQRLTAHKKIKENSSKEDELETLAE 119
      61 POKRTSKRYLHTLHESIKLTPFERERLNLQRLTAHKKIKENSSKEDELETLAE 120
Db
QY      120 EAIAGVPEVNIKESIGEVEFKICYEDENIIGVGGTLKDFLNSFTLLKQSSHCQEA 179
      121 EAIAGVPEVNIKESIGEELFKICYEDEHIIIGVGGTLKDFLNSFTLLKQSSHCQEA 180
QY      180 KGRLEDASILLCKEDDFLHYFFPPKRTTSLILPGIITKAAHVLETEVEVSLMPPC 239
      181 KGRLEDASILLCKEDDFLHYFFPPKRTTSLILPGIITKAAHVLETEVEVSLMPPC 240
Db
QY      240 FHDCEFEVNOPYLTVSVHMKSTPSPKPOSSLVPTSLCKTPEFHMDKMTILQ 299
      241 FHDCEFEVNOPYLTVSVHMKSTPSPKPOSSLVPTSLCKTPEFHMDKMTILQ 300
Db
QY      300 FCGNGIRLNNRRDFOGKPNFEFEFLITPKINOTFGSITMLNMQFVVRVRMDNSVKKS 359
      301 FCGNGIRLNNRRDFOGKPNFEFEFLITPKINOTFGSITMLNMQFVVRVRMDNSVKKS 360
Db
QY      360 SRVMDLKGOMIYVSSAILFLGSPCVDRLEDFTGRLGLYLSDIPIHNLADVVLIGEQA 419
      361 SRVMDLKGOMIYVSSAILFLGSPCVDRLEDFTGRLGLYLSDIPIHNLADVVLIGEQA 420
Db
QY      420 RADDGLKRRIGKTKATEAOHQAOLEEKKKTVDLLCSIFCEVAQOIMOGVQAKKESNV 479
      421 RADDGLKRRIGKTKATEAOHQAOLEEKKKTVDLLCSIFCEVAQOIMOGVQAKKESNV 480
Db
QY      480 TMLFSDIVGFTALICSCSPLOVITMLNALTFRDQCGELDYKVTETIGAYCVAGGLH 539
      481 TMLFSDIVGFTALICSCSPLOVITMLNALTFRDQCGELDYKVTETIGAYCVAGGLH 540
Db

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QY 540 KESTHVAOIALMALKMMELSDVMSPHGEPIKRIKIGHSGSVAGVGVKMPRYCLFGN 599
DB 541 KESTHVAOIALMALKMMELSHVEVSPHGEPIKRIKIGHSGSVAGVGVKMPRYCLFGN 600
QY 600 NVTLANFESCSVPRKINVSPTTYRLKDCGPFVTPSPRELPNPNSEIIGICHFLDA 659
DB 601 NVTLANFESCSVPRKINVSPTTYRLKDCGPFVTPSPRELPNPNSEIIGICHFLDA 660
QY 660 YQOGTNSKPCPKQKQVEDGNANFLGKASGID 690
DB 661 YQOGTNSKPCPKQKQVEDGNANFLGKASGID 691

RESULT 4
CYGA_RAT CYGA_RAT STANDARD; PRT; 730 AA.
AC 09WV14;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Guanylate cyclase soluble, alpha-2 chain (EC 4.6.1.2) (GCS-alpha-2).
GN GUCYL1A2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mistar Kyoto; TISSUE=Aorta;
RX MEDLINE=20571097; PubMed=11121588;
RA Koglin M., Behrends S.;
RT *Cloning and functional expression of the rat alpha(2) subunit of
RT soluble guanylyl cyclase.;
RL Blochum. Biochem. Acta 1494:286-289(2000).
CC -1- FUNCTION: HAS GUANYLYL CYCLASE ON BINDING TO THE BETA-1 SUBUNIT.
CC -1- CATALYTIC ACTIVITY: GTP -> 3',5'-cyclic GMP + diphosphate.
CC -1- ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE OF
CC MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES: SOLUBLE
CC FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
CC -1- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF109963; AAD42949.2; -.
DR HSSP; P19687; IAWN.
DR InterPro; IPR001054; G_cyclase.
DR Pfam; PF00211; guanylate_cyc; 1.
DR SMART; SM00044; CYC; 1.
DR PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.
DR PROSITE; PS00125; GUANYLATE_CYCLASES_2; 1.
DR Lysase; CGMP synthesis; Multigene family.
FT DOMAIN 519 646 GUANYLATE CYCLASE.
FT DOMAIN 50 72 ALA-RICH.
FT DOMAIN 64 72 POLY-ALA.
SQ SEQUENCE 730 AA; 81786 MW; B8D790BF81B8F9 CRC64;

Query Match 46.0%; Score 1651; DB 1; Length 730;
Best Local Similarity 49.2%; Pred. No. 1.le-107;
Matches 355; Conservative 106; Mismatches 196; Indels 64; Gaps 14;

QY 13 GECPEFSLA-----PGOVNNESSERAGSSSECKATVPICODIPKNIQEST----- 59
DB 27 GECPEFSLA-----PGOVNNESSERAGSSSECKATVPICODIPKNIQEST----- 59

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QY 60 POKTSRNVYLAHTLAESICKLIPPEPERLVALORTLA--KHKI-----KESRKL----- 109
DB 74 SKRAQRRNRVNLDSGESISLTLTAPSPQTHMLTKRLQYEHVIGYVROAKRNFHNS 133
QY 110 -----ERDFEKTIAEQVAVGVPEVVKESIGEVEFKICYEDENILGVGCT 158
DB 134 RCSSADHSNKEIEIDVSGILNCTANVLGKQEOIERHEFFKICDENRVRVAVGST 193
QY 159 LKDFLNSFTLLKQSSHQEA-GKRGRLDASITCLKEDFLVYVYFFPRTSLILPG 217
DB 194 LQDFPNGEDALLE--HRTSFGKQATLESFSLCKELPEGLTLNHPHHTVGPALG 250
QY 218 IIRAAHYLYETEVEV-SLMPPCPHNDCSEFVNOPYLLIYVHMSSTPSLSPKQSSLY 276
DB 251 MIKAAKRIYHLNVEVEQIEENKCSGSPSTNSCLFLKKECT-TQITKNIPQSTQ 309
QY 277 IPTSL-----FCTPPPHFMDKMTIILQGNIGIRLNRDRQKRNFEYELLTPK 330
DB 310 IPTDLRISINTFCRTFFFLMFDPNMVVLQIGEGRLKQI-RCDNHKKYLKFEDECEIYSPK 368
QY 331 INTFSGIMTILNMQFVVRVBRMNSYKSSRVADLKGOMIYIYESSALIFGSPCYDL 390
DB 369 VNAIFDRLYLRLSTPFYIRKPEASGDNEDKVEIKGMITHVESNHLIFLSSPCVDKL 428
QY 391 EDFTGRGLYLSDIPHNALRDVYLIGDQARAQDLKRLKATLQAHQALEEKKRT 450
DB 429 DELIGRGLHSDIPDHATRDVYLIGDQARAQDLKRLKATLQAHQALEEKKRT 488
QY 451 VDLICSTFCPCVAAQMLQGOVQAKKNSNTYMLFSDIYGFALISQCSPLQVITMLNLY 510
DB 489 VDLISITFCPCVAAQMLQGOVQAKKNSNTYMLFSDIYGFALISQCSPLQVITMLNLY 548
QY 511 TRFDQCGELDYVYETIGDAYCYVAGGLHKSQTHAVOIALMALKMMELSDVMSPHGE 570
DB 549 TRFHQCGFLDIYVERIGDAYCYVAGGLHKSQTHAVOIALMALKMMELSDVMSPHGE 608
QY 571 IIRKIGHSGSVPRKINVSPTTYRLKDCP 630
DB 609 IOMKIGHSGSVPRKINVSPTTYRLKDCP 668
QY 631 GFVTPSPRELPNPNSEIIGICHFLDAVQOGGINSKPCPKQKQVEDGNAN----FLCKA 686
DB 669 SFTFIPSPRELPNPNSEIIGICHFLDAVQOGGINSKPCPKQKQVEDGNAN----FLCKA 728
QY 687 S 687
DB 729 S 729

RESULT 5
CYGA_HUMAN CYGA_HUMAN STANDARD; PRT; 732 AA.
AC P33402;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Guanylate cyclase soluble, alpha-2 chain (EC 4.6.1.2) (GCS-alpha-2).
GN GUCYL1A2 OR GUC1A2 OR GUCSA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=92070494; PubMed=1683630;
RX Hatteneck C., Wedel B., Koesling D., Molkwitz J., Boehme E.,
RA Schultz G.;
RT *Molecular cloning and expression of a new alpha-subunit of soluble
RT guanylyl cyclase. Interchangeability of the alpha-subunits of the
RT enzyme.;
DB FEBS Lett. 292:217-222(1991).
RN [2]

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RP SEQUENCE FROM N.A. (ISOFORM ALPHA 2-1).
RA MEDLINE=95403342; PubMed=7673142;
RX Behrends S., Harteneck C., Schultz G., Koesling D.;
RT "A variant of the alpha 2 subunit of soluble guanylyl cyclase
RT contains an insert homologous to a region within adenylyl cyclases
RT and functions as a dominant negative protein.";
RL J. Biol. Chem. 270:21109-21113(1995).
CC -1- FUNCTION: HAS GUANYLYL CYCLASE ON BINDING TO THE BETA-1 SUBUNIT.
CC THE ALTERNATIVE SPLICED ISOFORM, ALPHA-2-1, ACTS AS A NEGATIVE
CC REGULATOR OF GUANYLYL CYCLASE ACTIVITY AS IT FORMS NON-FUNCTIONAL
CC HETERODIMERS WITH THE BETA SUBUNTS.
CC -1- CATALYTIC ACTIVITY: GTP -> 3',5'-cyclic GMP + diphosphate.
CC -1- ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE OF
CC MAGNESIUM OR MANGANESE IONS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA-2 (SHOWN HERE) AND
CC ALPHA-2-1; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: ALPHA-2 ISOFORM IS EXPRESSED IN FETAL BRAIN,
CC LIVER, COLON, ENDOTHELIDUM AND TESTIS, WHILE THE ALPHA-2-1 FORM
CC IS EXPRESSED ONLY IN LIVER, COLON AND ENDOTHELIDUM.
CC -1- MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLYL CYCLASES: SOLUBLE
CC FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
CC -1- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
CC FAMILY.
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CC -----
DR EMBL; X63282; CA444921.1; -;
DR EMBL; Z50053; CA90393.1; -;
DR PIR; S18325; S18325.
DR HSSP; P19687; 1AMN.
DR Genew; HGNC:4684; GUCY1A2.
DR MIM; 601244; -;
DR InterPro; IPR001054; G_cyclase.
DR Pfam; PF00211; guanylate_cyc; 1.
DR SMART; SM00044; CycC; 1.
DR PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.
DR PROSITE; PS50123; GUANYLATE_CYCLASES_2; 1.
KW Lyase; GMP synthesis; Multigene family; Alternative splicing.
FT DOMAIN 521 648 GUANYLATE CYCLASE.
FT DOMAIN 51 76 ALA-RICH.
FT DOMAIN 51 58 POLY-ALA.
FT VARSPLIC 612 612 Q -> QPQRMELLSFVSIQVLPDQHOSETDLGTER
FT FT (IN ISOFORM ALPHA 2-1).
SQ SEQUENCE 732 AA; 81749 MW; 79465A7D3FE52DB7 CRC64;
Query Match 45.5%; Score 1635; DB 1; Length 732;
Best Local Similarity 49.4%; Pred. No. 1.5e-106; Indels 58; Gaps 15;
Matches 355; Conservative 106; Mismatches 200;
QY 13 GECFSLTA-----PGQVNESSEEAAGSSCQATVPICQDIPKNIQESLPQRTS 65
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 27 GECVLSRLCNMGNSPRG--PLERSPAAAAA--AAPAPPAASAAAAAATAGARVQR 81
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 66 RSRVYLHTLASICKLIFPEEFERLVALQRTLA--KHKI--KESRKSL----- 109
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 82 RRRVNDLSIGESIRLTPSPQTIQQLTKLQYEHGVIGVRAQKFNHNSNRCYAD 141
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 110 -----ERRDFEKRTIAEQAVAGVVEVYKESIGEVNVCICVEDNNITGVGGTLDKELN 164
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 142 HSNKEETEDVSGIIQCTANILGLFEEIQKRGEFFNICHEMRNVRANVGATQDDEFN 201
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 165 SEFTLKSSQCOEA-GRGRLEDAASIICTKDEDFLHYVEFFPKRTSLIPIGIIKAA 223
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 202 GFDALIE---HRTISFGKQATLLESFSLCKELPBEETLMDHTFHPHHIYGVFAMIGMIKAG 258
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

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OY 22 HVLVEVEVSLAMPCEFHND--CSEFVNOP--YLLYSVHKMSYKPSLSPEKPOSSLVYP 278
Db 259 KRIYRLDVEVEYOVA-----NEKLSCD-VSPNGKSCSLTILFECENTNIMKMLPGQYQVP 313
OY 279 TSL-----FCKTFPEHMFEDKMTILOFGNIRRLANRDRFOGKNPEEYFELITPEKIN 332
Db 314 ADRISSINTECFRAFPEHLMFEDPSMSVYLQJEGELRKQOL-RCDPHNKVLKPEDCFEIVSPKN 372
OY 333 QTESGIMTLMNQFYVRYRRMDSNYSKKSRYVMDLGGOMIITYESSAILIFLQSPCVYDLE 382
Db 373 ATERRVLLRSTFVYLRKPEASGSSNNDRKVEVNGQMIHVPESSNIIFFLQSPCVYDLE 432
OY 393 FTFRGTYLSDPIPHNALRDVYLVLGEQARAODILKRLKILKATLEQAHOALEEKRKTYD 452
Db 433 IMRGJHLSDPIPHNADTRVYLVLGEQAKAODILKRLKMDKATLERTQALAEKKRTYD 452
OY 453 LLSISRPCVEVAOOLMOGOVYOAKRSNTMLFSDIVGTALICSOCSPLQVITMLNLYTR 512
Db 493 LKLSIFPGVDVAOOLMOGOVOYAKRDDVYMLFSDIVGTALICAOCTPMQVISMNELYTR 552
OY 513 FDOCCSELIVYKKEITIGDAYCYVAGGLHKEPSDTHAVOILMLKMMELSDVMSPHGEPIK 572
Db 553 FDIQCCGRDIYKKEITIGDAYCYVAAGLHRSLSCHAPILMLKMMELSEVLTITDGRPIQ 612
OY 573 MRIGLHSGYFAGVGVCKMRYCLFGNNVTLANKFESCVCPRKINVSPYYRLILKDCPGF 632
Db 613 MRIGIHSGSYLAGVGVCKMRYCLFGNNVTLANKFESGSHPRRIIVSPYYTQOLKRESEF 672
OY 633 VETPRSEELPRPPEISPEIGICHLIDAYQOGINSKCPQKMDVEGNN-----PLGKAS 687
Db 673 TETPRSEELPRPPEISPEIGICHLIDAYQOGINSKCPQKMDVEGNN-----PLGKAS 687

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RESULT

ID	CYGH_DROME	STANDARD;	PRT;	683	AA.
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DT 01-FEB-1995 (Rel. 31, Created)

DT 16-OCT-2001 (Rel. 40, Last ann

GN GYC-ALPHA-99B OR GYC-ALPHA-63A OR GYC OR DGCL.

OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

R_N	[1]
R_N	[1]

RC STRAIN=Canton-S; TISSUE=Head;

RA Yoshikawa S., Miyamoto I., Aruga J., Furuichi T., Okano H.,

RT "Isolation of a *Drosophila* gene encoding a head-specific guanylyl]

RL J. Neurochem. 60:1570-1573 (1993).

CC MAY BE REQUIRED FOR ENZYME ACTIVITY.

```
CC -I - SUBUNIT: DIMER (PROBABLE).
```

CC - TISSUE SPECIFICITY: HEAD, WHERE IT IS PREFERENTIALLY EXPRESSED IN

CC -1- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASES

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CC		EMBL; S57126; AAB25820.1; ..	
DR	HSP: JH0810; JH0810.		
DR	P19687; IANM.		
DR	FlyBase; FBgn0013972; Gyc-alpha-99B.		
DR	InterPro; IP001054; G_cyclase.		
DR	pfam; PF00211; guanylate_cyc; 1.		
DR	SMART; SM00044; CYCC; 1.		
DR	PROSITE; PS00452; GUANYLATE CYCLASES.1; FALSE_NEG.		
DR	PROSITE; PS0125; GUANYLATE CYCLASES.2; 1.		
DR	Lysase; CGMP synthesis; Multigene family; vision.		
KW	DOMAIN 465 591		
FT	SEQUENCE 683 AA: 75906 MW; 12D67C4B79A07C8D CRC64;		
SQ			
Query Match	27.2%; Score 976.5; DB 1; Length 683;		
Best Local Similarity	37.3%; Pred. No.1,3e-60;		
Matches 244;	Conservative 116; Mismatches 211; Indels 83; Gaps 20;		
OY	58 SLPOKTRSRVYLHTLAETISCKILPEPERLNVALQRTIAK-----HKIK--BSR 106		
DB	27 ALDEDELDDALTLTHLMALIOQLAPSENEDINTAVTSLVAKYRONMPNIHKLDPOTF 86		
OY	107 KSLREDEPKTAIE-----DAVAAGVVEVYKEISAGEVRKICEE-DENLTGVVGSTL 159		
DB	87 KSCANVDIADIQELLKMDKESAEIIY-----LLGSELLTCCTGTITIERAFRCIGTDL 141		
OY	160 KDFLNFS--TLKQSSHCOEAGRGRLEDAASILCDKREDDFLVHYFFPRTSLIP 216		
DB	142 QEFGLSLGGVDYLR----LQED---VTDTGFVCAGEGE---LIPTSERVIAMLL 189		
OY	217 GIIRKAANVLTEVEVSEVLMPPCFINDCSEPNQYLL-----SYHMSTRPSLSPRQ 272		
DB	190 GSLKALTMLKIVDNINIKIEP---EKCPASISPLAQGOQLPDHADGSSTSVMKTIPE 245		
OY	273 -----SSLYPTSLFCFTEPFHFMFKDWTILOFGNGIRIRLARNDFOGKNFEE 322		
DB	246 TVQRNSNNASDLQMNSSSFCEMFPMWHIIMNQELVOLGNGFSKLY-----KPYAD 298		
OY	333 -----YFEILTFR-INOTFSGIATMLMOGFVNRVRMDNSVKSSRYMDLKGMITYI 374		
DB	299 FGCAQTTFYEDRPKRPGILTMKFPRDIYRRYYTFELLGINPPPAADVPAALGLEIKGMVHC 358		
OY	375 ESSAILFYGSCVDLEDFTGRCGLTSDIPHNALRDVNLIGEORADDGLKKRLGRIKA 434		
DB	359 ESNSTLIFGSPFDLDGLTGCGLFISDIPLDHAREVILVGEORADGGLRRRKDKTKN 418		
OY	435 TLEQAHAOLEEKKKTVDLCISFECVEAAOLMOGOVAAOKFSNVMTLFSDIYGTAIC 494		
DB	419 SIEEANSVTERKKRNVSLLHLIFAPAETAEKMGSSIDATYPDVTLIFSIDIYGTSIC 478		
OY	495 SOCSPLOYITMNLTYRFDOCCGLDYVYKETIGDACVAGGLHKS--DTHAVQIALM 552		
DB	479 SRAPFPVISMLEGIKYKDFDECDFDYVYKETIGDACVASGLHRASIYAHR--CLD 535		
OY	553 ALKMMELDEVMSPGPBPICKRIKGSHSGSVAGVVGMPCPYCLFGNNVTLANKRESQSV 612		
DB	536 GLKMIDACSKHITHDGEQIKKRIGHGTGYLAGVYGRMPRYCLFGHSVTIANKRESSE 595		
OY	613 PKRIWSTYTRILKDCPGPVF--TPRSRELPFNPBEIIG---ICGFIDAYQ 661		
DB	596 ALKINWSPTTKDMLTKRHGFEFELOPRDSPSLPKREFPN--PGGETCYFLESFR 647		
RESULT 7			
CYGL_RAT	STANDARD:	PRT:	619 AA.
AC	P20595;		
DT	01-FEB-1991 (Rel. 17, Created)		
DT	01-FEB-1991 (Rel. 17, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Guanylate cyclase soluble, beta-1 chain (EC 4.6.1.2) (GCS-beta-1)		
DE	(Soluble guanylate cyclase small subunit).		
GN	GUCY1B1 OR GUCY1B3 OR GUC1B3.		

CC CC Rattus norvegicus (Rat).
OC Euryotia; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OK NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=69087429; PubMed=2905128;
RA Nakane M., Saheki S., Kuno T., Ishii K., Murad F.;
RT "Molecular cloning of a cDNA coding for 70 kilodalton subunit of
RL soluble guanylate cyclase from rat lung."
RC Biochem. Biophys. Res. Commun. 157:1139-1147(1988).
CC -1 CATALYTIC ACTIVITY: GTP -> 3',5'-cyclic GMP + diphosphate.
CC -1 ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE OF
CC MAGNESIUM OR MANGANESE IONS.
CC -1 SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1 SUBCELLULAR LOCATION: Cytoplasmic.
CC -1 TISSUE SPECIFICITY: LUNG AND BRAIN.
CC -1 MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES: SOLUBLE
CC FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
CC -1 SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
CC FAMILY.

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CC -----

DR EMBL; M23562; AAAA1204.1; -.
DR PIR; A31871; OYTB1.
DR HSP; P16068; IAMN.
DR InterPro; IPR001054; G_cyclase.
DR Pfam; PF00211; guanylate_cyc; 1.
DR SMART; SM00044; CYC; 1.
DR PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.
DR PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
DR LYase; cGMP synthesis.
FW FT DOMAIN 421 554
SQ SEQUENCE 619 AA; 70477 MW; BCC9850DE4504226 CRC64;

Query Match 22.1%; Score 795; DB 1; Length 619;
Best local similarity 34.3%; Pred. NO. 5.2e-48;
Matches 210; Conservative 100; Mismatches 225; Indels 78; Gaps 15;

QY 89 LNVALQTLAKHKIKESRKSLERE-----DEKKT--IAEQAAAGPYVE 130
DB :|::||::||::||::||::||::||::||::||::||::||::||:
Y 5 VNHLELTLYIRNGPEVWEDIKKEAQDQEGFLVRIYDHSTKYDLVAASRYLNAG 64
DB :|::||::||::||::||::||::||::||::||::||::||::||:
QY 131 VINESAGEEYFKICEED-ENLGAVGCTLKDPINSTYLTKOSSHQGEAGKRLEDAS 169
DB :|::||::||::||::||::||::||::||::||::||::||::||:
Y 65 ELLDMFEKMFVFEEQESGYDTTLKVLSSNVREFQLNDAL----HDHATIPYGMAPS 119
DB :|::||::||::||::||::||::||::||::||::||::||::||:
Y 190 ILCLDKR-DPFLAHYFYFPKRTSLILPGILKAHAHYLFTEYEVSIM---PPCFHNDC 244
DB :|::||::||::||::||::||::||::||::||::||::||::||:
Y 120 FRCTDAKRGKLIIHYSEREGLDYIGLIKRYAQIHGTETIDMKYIQGRSECHQTG- 178
DB :|::||::||::||::||::||::||::||::||::||::||::||:
QY 245 SEPANOYLYLVSMKSTRPS-----LSPKFPOSILVIPSLFRCKTFPHFMDDKD 236
DB :|::||::||::||::||::||::||::||::||::||::||::||:
Y 179 -----FLIEEKSKKEDEFDLDFREENGTODSRISPYT-FCKAPFHIFDRDL 227
DB :|::||::||::||::||::||::||::||::||::||::||::||:
QY 297 TLLOFGNGIRLMRRPOFKRPNFEYEFELTPRINTFGSGMTMLMQGVVVVRMDNS 356
DB :|::||::||::||::||::||::||::||::||::||::||::||:
Y 228 VYVQCNAITRVLPOLD-PGRCSLTSFSLVLRPHIDSFGILISHIVTVVLSKESGLD 286
DB :|::||::||::||::||::||::||::||::||::||::||::||:
QY 357 VKR-----SSRYMDLKGMYIVVESAILFLGSPCVDRLDEFNGLYLSDPIH 406
DB :|::||::||::||::||::||::||::||::||::||::||::||:
Y 287 VEKLECEDELTAIGEISCLRKGGMYIVPEADSIILFCSPVMNLDDTRGRGLYSIDIPH 346
DB :|::||::||::||::||::||::||::||::||::||::||::||:
Y 407 MALRDVYLIEQARADGKKRGRGLKATLEQAQHAALEEKKRTVDLSCIFCEYAQOL 466
DB :|::||::||::||::||::||::||::||::||::||::||::||:
Y 347 DARDVDLVLEGREERKYLQOEILEITDRDQLRLALEDEKRTVDLVLVSLPPSAANEL 406
DB :|::||::||::||::||::||::||::||::||::||::||::||:


```

RL FEBS Lett. 304:83-88(1992).
RN RP SEQUENCE FROM N.A. (ISOFORM HSGC-2).
RC RA Ganssems Y., Brouckaert P., Piers W.;
RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 337-545, AND ALTERNATIVE SPLICING.
RC TISSUE-LUNG.
RX MEDLINE=92008652; PubMed=1680753;
RA Chhajlani V., Fraendberg P.-A., Ahlner J., Axelsson K.L.,
RT Wikberg J.E.S.;
RT "Heterogeneity in human soluble guanylate cyclase due to alternative
RT splicing.";
RL FEBS Lett. 290:157-158(1991).
CC -1- CATALYTIC ACTIVITY: GDP = 3',5'-cyclic GMP + diphosphate.
CC -1- ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE OF
CC MAGNESIUM OR MANGANESE IONS.
CC -1- SUBUNIT: HEMERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, HSGC-1 (SHOWN HERE) AND HSGC-2;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES: SOLUBLE
CC FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
CC -1- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
CC FAMILY.
CC -----
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CC -----
DR EMBL; X66533; CAA47144.1; -.
DR EMBL; AF020340; AAB94877.1; -.
DR PIR; S23097; S23097.
DR HSSP; P16068; 1AMN.
DR GeneW; HGNC:4687; GUCY1B3.
DR MIM; 139397; -.
DR InterPro; IPR001054; G-cyclase.
DR Pfam; PF00211; guanylate_cyc; 1.
DR SMART; SM00044; CYCC; 1.
DR PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.
DR PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
DR Lyase; cGMP synthesis; Alternative splicing.
FT DOMAIN 421 554 GUANYLATE CYCLASE.
FT VAAPSPIC 393 425 MISSING (IN ISOFORM HSGC-2).
SQ SEQUENCE 619 AA; 70514 MW; 21EAE660DE02AA1 CRC64;
Query Match 22.0%; Score 789.5; DB 1; Length 619;
Best Local Similarity 35.1%; Pred. No. 1.3e-47;
Matches 207; Conservative 96; Mismatches 219; Indels 67; Gaps 15;
DY 101 KIKESRSLSREDEKRTIAGQAVAGPY-----EYIKESLGEVFKICYEED-ENILG 153
DY 30 QLDSEGGLFVRIIYDDSKTYDVLVAASKVLTLMNGEIL-QWGFMPFVFCQESGYDILR 88
DY 154 VGGTLLDFLNFSTLLKQSHCOEAKRGRLDEASTICLDKE-DDFLHYVYFPFKRTS 212
DY 89 VLGSNVAFELQNDAL-----HDLATITYGMRAPSRFCDAEKGKGLILHYISERGLQ 143
DY 213 LILPGITKAHAHVLYETEVEVSLM-----PCFHNDCSEFVNQPYLLYSVHKSKYRPS-- 265
DY 144 DIVIGIKITVAQOIHGFEIDMKVYIQGNNEEDHQ-----FLIEKESKEDFY 192
DY 266 -----LSPSKRQSSLVLPSTLFCCKTFPFHFEDKMTILQFGNCIRLMANRDFQKPNF 320
DY 193 EDLDREFENQTESRISPYT-FCKAFFPHFIIDRLVLTVOCGNAIYEVLPQLQ-PGNCSTL 250
DY 321 EEVFEILTPTKINQFSGIMTLMNQGVVAVRRMDSYRK-----SRVMDLKGOM 370

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Db	251	LSVSVLPHADISPHGILSHINIFVLRKSEGLDVEKLECEDELTGTEISCLRLKGM	310
Qy	371	IYIYESSALLFLSGCVNRLEDFTGRGILYSLDIPRHNALRQVYLIGEARADGLKRLG	430
Db	311	YLLPSPADSLFLVCSVMNLDDTLRRGLYSLDIPLDHTRDLVLLGEQFRRYKLTGLE	370
Qy	431	KLKATLEQAOALBEKKKTYDLLCSIPCEVAOOLMGQVQAKFNSVMTLFEIDYGF	490
Db	371	ILTRQLQTLTALDEKKKTYDLYSVLPSPVANLRKRPVAKRQVNVITLFGIYGF	430
Qy	491	TAISQCS---PLQVITMLNALTTRFDQCGELD---VYVETIGDAIVCAGLHKESD	543
Db	431	NAFCSKHSAGGAKNIWMLNDLYTRFDPTLLDTSRKNPVEYVETIGDVMVSGPEPCI	490
Qy	544	THAVOIALMKMELSDVNSPGEPIKMGILGHSVSPFAGVGVKAPRYCLFGNNVL	603
Db	491	HHASICHALDMHEIAGQVQVDSVQITIGITGHEVTVGVICQRPKICLFGNTVNL	549
Qy	604	ANFESCSVPKRVNSPTTYRLDKDCPGFVETPNRSREELPNPSPSEIPG	652
Db	550	TSRETTGEGKRIINSEYTYRCL-----MSPENDSQFLEHHRG	588

RESULT 10

ID	CYCL2_RAT	STANDARD:	PRT:	682 AA.
AC	P22717;			
DT	01-AUG-1991 (Rel. 19, Created)			
DT	01-AUG-1991 (Rel. 19, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Guanylate cyclase soluble, beta-2 chain (EC 4.6.1.2) (GCS-beta-2).			
GN	GUCY1B2.			
OS	Rattus norvegicus (Rat).			
OC	Eumetazoa; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.			
OX	NCBI_Taxid=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Kidney;			
RX	MEDLINE=91105012; PubMed=1980215;			
RA	Yuen P.S.T., Potter L.R., Gathers D.L.;			
RT	*A new form of guanylyl cyclase is preferentially expressed in rat			
RT	kidney.*;			
RL	Biochemistry 29:10872-10878(1990).			
CC	-1- CATALYTIC ACTIVITY: GMP -> 3',5'-cyclic GMP + diphosphate.			
CC	-1- ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE OF			
CC	MANGNESTIUM OR MANGANESE IONS.			
CC	-1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.			
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic.			
CC	-1- TISSUE SPECIFICITY: KIDNEY AND LIVER.			
CC	-1- MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES: SOLUBLE			
CC	FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.			
CC	-1- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE			
CC	FAMILY.			
CC	-----			
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@lsb-sib.ch).			
CC	-----			
DR	EMBL: M57507; AAA41207.1; .			
DR	PIR: A36228; OYTB2.			
DR	HSSP: P19687; IAWN.			
DR	InterPro: IPR001054; G_cyclase.			
DR	InterPro: IPR001230; Prenyl_site.			
DR	PFam: PF00211; guanylate_cyc; 1.			
DR	SMART: SM00044; CYC; 1.			
DR	PROSITE: PS00452; GUANYLATE_CYCLASES_1; 1.			
DR	PROSITE: PS50125; GUANYLATE_CYCLASES_2; 1.			
DR	Lyase; cGMP synthesis.			


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FT DOMAIN 408 536 GUANYLATE CYCLASE.
SQ SEQUENCE 682 AA; 76196 MW; 98C173C1ACCT715 CRC64;
Query Match 21.6%; Score 774.5; DB 1; Length 682;
Best Local Similarity 32.6%; Pred. No. 1.6e-46;
Matches 190; Conservative 107; Mismatches 204; Indels 81; Gaps 10;
OY 129 VEVIKESIGEVEFKICYED-ENIGVVGTLKDFLNSFTLLKQSSHOEAKRGRLD 187
DB 1 MEALIKLGEYEFKCKSKSGYDRMLRTLGNGLTERIENDAL-----HSYALSYQEMNA 55
OY 188 ASILCLKEDDFLHYFFPKRTSLILPGITKAAAHVLEVEVSLMPCFHCDSSEF 247
DB 56 PSFVREEGADGAMLLHYSDRGILCHIVPGIIEAVALKDFDIDVAMSTIL-----DMNEE 109
OY 248 V-----NOPYLYSVHMKSTKP--SLSPSKQSS----- 274
DB 110 VERGKREHYVFLVYQAKHROIRGAKASRPOGSESDQADQALOGTLRMKRYINIPVC 169
OY 275 -----LVIPISLFCCKTFPHFMDKMTILQFG 302
DB 170 PGEKSHSTAVRASVLFGRGLDTPQPYPERLWVEEVEFCDAFPFHIFEDALVAKQAG 229
OY 303 NGIRLIMRDEQGRNFEVEFEITPKINOTFSSIMTLNQFVVRAR-WDNSYKSS 361
DB 230 VNIQKVPGLILQ--KFAIDEFYSLHPVTENISSICKFISQFVLKTRKEMPRARSQ 288
OY 362 RVMDKGMIVIVESSALIFLSCPCVDRLEDFTRGLYISDPINHALDVLVIGEOARA 421
DB 289 PMLKRGOMIMNESLRCHIFMCSPPVRSIQELEESKMHSDIAPDTRDLILNQRLA 348
OY 422 QDGLKRLKGLKATLEQAHAOLEEKKRTVDLCSIFPCEVAQOLMOGOVVOAKKFSNYT 481
DB 349 EMELSCQEKKEEKLRLVSNHLAIEKKTEITLLYMLPEHVANOQKEGKVAAGEFECT 408
OY 482 MLFSDIVGFTALCSQSPLOVYTMNALYTRDQCGGELDYKVFETIGDAYVAGLAK 541
DB 409 ILFSVVFPTNCAACEPIQIVNMLNSMSKPDRLTSVHDYKVFETIGDAYVAGVGPVP 468
OY 542 SDTHAVOITMALMKMETLSDVEVSP-HGEPIRMIGLSGVSFAGVGVKMRVYCLFGNN 600
DB 469 VESHAQVAVNPAFALGRISAKVEYVNPVTEGPIQIRGIRHGPVLAGVGDKMRVYCLFGDT 528
OY 601 VTLANKFESCVPRKINVSPTTYRLKDCGPFVTPRSREL 642
DB 529 VNTASRMESHGIPSKVYHLSPFAHRAKLN-KGFEIVRGEIEV 569

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RESULT 11

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CYG2_HUMAN STANDARD; PRT; 617 AA.
AC 075343; Q9NZ64;
DT 15-JUL-1999 (Rel. 38, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Guanylate cyclase soluble, beta-2 chain (EC 4.6.1.2) (GCS-beta-2).
GN GUCY1B2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A., AND REVISION TO 175.
RC TISSUE=Kidney;
RX MEDLINE=20241821; PubMed=10777682;
RA Behrends S., Vehse K.;
RT "The beta(2) subunit of soluble guanylyl cyclase contains a
RT human-specific frameshift and is expressed in gastric carcinoma.";
RL Biochem. Biophys. Res. Commun. 271:64-69(2000).
[2]
RP SEQUENCE OF 95-257 FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=99107820; PubMed=9889008;

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RA Behrends S., Kazmierczak B., Steenpa A., Knauf B., Bullerdick J.,
RA Scholz H., Elberg H.;
RT "Assignment of GUCY1B2, the gene coding for the beta2 subunit of human
RT guanylyl cyclase to chromosomal band 13q14.3 between markers D13S168
RT and D13S155."
RL Genomics 35:126-127(1999).
CC -1- CATALYTIC ACTIVITY: GTP -> 3',5'-cyclic GMP + diphosphate.
CC -1- ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE OF
CC MAGNESIUM OR MANGANESE IONS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES: SOLUBLE
CC FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
CC -1- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
CC FAMILY.
CC -----
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CC -----
DR EMBL; AF038499; AAD09440.2; -.
DR EMBL; AF218383; AAF6105.1; -.
DR HSSP; P19687; 1ANM.
DR GENE; HGNC:4686; GUCY1B2.
DR MIM; 603695; -.
DR INTERPRO; IPR001054; G_cyclase.
DR Pfam; PF00211; guanylate_cyc; 1.
DR SMART; SM00044; CYCC; 1.
DR PROSITE; PS00452; GUANYLATE_CYCLASES_1; FALSE_NEG.
DR PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
KM lyase; GMP synthesis.
FT DOMAIN 391 519
SQ SEQUENCE 617 AA; 70367 MW; 1B6C965CAB9A5E3E CRC64;
Query Match 19.7%; Score 708; DB 1; Length 617;
Best Local Similarity 31.3%; Pred. No. 6.1e-42;
Matches 179; Conservative 100; Mismatches 191; Indels 102; Gaps 12;
OY 149 ENILGVGGLKDFLNSFTL-----LKQSSHOEAKRGRLDASTILCLDKEDD 198
DB 5 DMLRTLGNGLMEFTENDALHSYALSYQEMNAPSFREVGADKM----- 51
OY 199 FLHYVFFPKRTSLILPGITKAAAHVLEVEVSLMPCFHCDSSEVNP----- 251
DB 52 FLH--VYSDRGLCHIVPGIIEAVALKDFDIDVIMDIL-----DMNEVEVTKREHYV 103
OY 252 -YLKSVH--MKSTKP----- 264
DB 104 FLIVQAKHKKMKTKPRKLRDQSGMERQEOALQAAFLKKEKYLIVNSACPYSKSHVDYR 163
OY 265 -----SLSPSKQSSLVIPISLFCCKTFPHFMDKMTILQFGNGIRIMNR 312
DB 164 SIYFEGKHLMTFPIYPE-RLMIEEKTEFCNAFPFHIFEDSLQKARVNIQKVPGL 222
OY 313 DQGRPNFEVEFEITPKINOTFSSIMTLNQFVVRARMSYKSSR-VMDLKGOMI 371
DB 223 QFO-NIQDEYFSILHPVTENIFSRIRISQFVLKTRKEMPRAMOSRTTLKLOGMI 281
OY 372 YIVESSALIFLSCPCVDRLEDFTRGLYISDPINHALDVLVIGEOARAQDGLKRLGK 431
DB 282 WMSNMCMWYLCSPKRSIQELEELNMHLSIAPDTRDLILNQRLAIELSNOLR 341
OY 432 LKATLEQAHAOLEEKKRTVDLCSIFPCEVAQOLMOGOVVOAKKFSNYTMLSIVGFT 491
DB 342 KKEELQVLSKHLAIEKKTEITLLYMLPEHVANOQKEGKVAAGEFSCITLFSVYET 401
OY 492 AICSCSPLOVYTMNALYTRDQCGGELDYKVFETIGDAYVAGLHKESTHAYOVAL 551
DB 402 NICTACEPIQIVNMLNSMSKPDRLTSVAHVYKVFETIGDAYVAGVGPVIGNHAQVAN 461

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QY 552 MALKMELSDVSNP-HGEPIKMRIGLHSGSVFAGVGVKMPRYCLGNNTYANKPESC 610
 DB 462 FALGMRISAKVETNPVGEPIQLRVGHTGSPVLADYGDKMPRYCLGDTYNTASRRESH 521
 QY 611 SVPRKIVSPPTTYRLKDCPGFVFTPRSREL 642
 DB 522 GLPKRVHLSPTAYRALKN-OGFKTIERGELEV 552

RESULT 12
 ANPB_BOVIN STANDARD: PRT: 1047 AA.
 ID ANPB_BOVIN STANDARD: PRT: 1047 AA.
 AC P46197;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Atrial natriuretic peptide receptor B precursor (ANP-B) (ANPRB) (GC-B) (guanylate cyclase) (EC 4.6.1.2) (NPR-B) (Atrial natriuretic peptide B-type receptor).
 GN NPR2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913.
 RN [1]
 RP SEQUENCE FROM N.A.
 RP TISSUE=Brain;
 RX MEDLINE=9514785; Pubmed=7845391;
 RA Fenrick R., Babinski K., McNICOLL N., Therrien N., Drouin J., de Lean A.,
 RT "Cloning and functional expression of the bovine natriuretic peptide receptor-B (natriuretic factor R1c subtype).";
 RL Mol. Cell. Biochem. 137:173-182(1994).
 RN [2]
 RP SEQUENCE OF 551-1047 FROM N.A.
 RP TISSUE=Retina;
 RX MEDLINE=93371497; Pubmed=8103329;
 RA Simmler B.E., Zubov D.V., Abdulaev N.G.;
 RT "Detection of expression of a membrane form of the guanylate cyclase type of GC-B in cattle retina (letter).";
 RL Bioorg. Khim. 19:682-685(1993).
 CC -1- FUNCTION: RECEPTOR FOR ATRIAL NATRIURETIC PEPTIDE. HAS GUANYLATE CYCLASE ACTIVITY ON BINDING OF LIGAND. THE ACTIVATION ORDER SEEMS TO BE CNP > BNP > ANP.
 CC -1- CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + diphosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- MISCELLANEOUS: THERE SEEM TO BE AT LEAST THREE ANP RECEPTORS: TWO WITH GUANYLATE CYCLASE ACTIVITY (ANP-A AND ANP-B) AND ONE (ANP-C) WHICH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF ANP FROM THE CIRCULATION WITHOUT A ROLE IN SIGNAL TRANSDUCTION.
 CC -1- SIMILARITY: SOME SIMILARITY WITH CONSERVED REGION OF CATALYTIC DOMAIN OF PROTEIN KINASES.
 CC -1- SIMILARITY: BELONGS TO ADENYL CYCLASE CLASS-4/GUANYL CYCLASE FAMILY
 CC -1- SIMILARITY: CONTAINS 1 PROTEIN KINASE-LIKE DOMAIN.
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 CC -----
 CC EMBL: L26359; AAC41619.1; -
 CC EMBL: X66865; CAA47334.1; -
 DR HSSP: Q02846; IAWL.
 DR InterPro: IPR001828; ANP_receptor.
 DR InterPro: IPR000719; Euk_kinase.
 DR InterPro: IPR001054; G_cyclase.
 DR InterPro: IPR001170; Ntpep_receptorin.

DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00211; guanylate_cyc; 1.
 DR Pfam; PF01094; ANP_receptor; 1.
 DR PRINTS: PR00255; NATPEPTIDER.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR SMART; SM00044; CTCG; 1.
 DR PROSITE; PS00458; ANP_RECEPTORS; 1.
 DR PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.
 DR PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW Receptor; Transmembrane; Glycoprotein; Phosphorylation; Lyase;
 KW cAMP_synthetis; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 1047
 FT DOMAIN 23 458
 FT TRANSMEM 459 478
 FT DOMAIN 479 1047
 FT DOMAIN 513 786
 FT DOMAIN 861 991
 FT DISULFID 75 101
 FT DISULFID 439 439
 FT DISULFID 448 448
 FT CARBOHYD 24 35
 FT CARBOHYD 161 161
 FT CARBOHYD 195 195
 FT CARBOHYD 244 244
 FT CARBOHYD 277 277
 FT CARBOHYD 349 349
 FT CONFLICT 958 958
 SQ SEQUENCE 1047 AA; 117145 MW; 1A381AD0F22D84F CXC64;
 Query Match 12.8%; Score 460; DB 1; Length 1047;
 Best Local Similarity 41.9%; Pred. No. 2,6e-24;
 Matches 113; Conservative 39; Mismatches 76; Indels 42; Gaps 6;
 QY 411 DVVLIGEQARAOD-----GLKRLRGK-----LKATLEDA 439
 DB 760 EYLLMERCAADPAERPDGQIKGFIIRNRKGGTSTIDNLLRMEQYANNLEKLYEER 819
 QY 440 HQALEEKKRKYVLLCSIFCEVAQOLMOGVQAKFSNVMTLFSIDYGFATGSCSCP 499
 DB 820 TOAYLEKRAEALYQILPHSAEDLKEGYQALAFSVITYFSDYGFATLSAESP 879
 QY 500 LQVITMLNLYTRFDQCGELDYKVTIGDAYCVAGI-HKESDTHAVQIALMAKME 558
 DB 880 MQVYTLNLDYTCFDALINDFDYKVTIGDAYVYVSGLPGRNGRHAPEIARMALAL- 938
 QY 559 LSEVWS-----PHEPIKMRIGLHSGSVFAGVGVKMPRYCLGNNTYANKPESC 612
 DB 939 --DAVSSFRIHRPH-DQLRLRGVHTGPGACGVGLKMPRYCLGDTYNTASRRESNCO 995
 QY 613 PRKIVSPPTTYRLKDCPGFVFTPRSREL 642
 DB 996 ALKIHVSSTTKDALDELGCPLERGDYEM 1025

RESULT 13
 ANPB_HUMAN STANDARD: PRT: 1047 AA.
 ID ANPB_HUMAN STANDARD: PRT: 1047 AA.
 AC P20584; Q9D050; Q60871;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Atrial natriuretic peptide receptor B precursor (ANP-B) (ANPRB) (GC-B) (guanylate cyclase) (EC 4.6.1.2) (NPR-B) (Atrial natriuretic peptide B-type receptor).
 GN NPR2 OR ANPRB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]

RESULT 14
ANP_RAT STANDARD; PRT: 1047 AA.

AC P16067;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Atrial natriuretic peptide receptor B precursor (ANP-B) (ANPRB) (GC-B)
DE (Guanylate cyclase) (EC 4.6.1.2) (NPR-B) (Atrial natriuretic peptide B-type receptor).
GN NPR2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=69376566; PubMed=2570641;
RA Schulz S., Singh S., Bellet R.A., Singh G., Tubb D.J., Chin H., Garbers D.L.;
RT "The primary structure of a plasma membrane guanylate cyclase demonstrates diversity within this new receptor family.";
RL Cell 58:1155-1162(1989).
CC -1- FUNCTION: RECEPTOR FOR ATRIAL NATRIURETIC PEPTIDE. HAS GUANYLATE CYCLASE ACTIVITY ON BINDING OF ANP. SEEMS TO BE STIMULATED MORE EFFECTIVELY BY BRAIN NATRIURETIC PEPTIDE (BNP) THAN BY ANP.
CC -1- CATALYTIC ACTIVITY: GTP -> 3',5'-cyclic GMP + diphosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- MISCELLANEOUS: THERE SEEM TO BE AT LEAST THREE ANP RECEPTORS: TWO WITH GUANYLATE CYCLASE ACTIVITY (ANP-A AND ANP-B) AND ONE (ANP-C) WHICH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF ANP FROM THE CIRCULATION WITHOUT A ROLE IN SIGNAL TRANSDUCTION.
CC -1- SIMILARITY: SOME SIMILARITY WITH CONSERVED REGION OF CATALYTIC DOMAIN OF PROTEIN KINASES.
CC -1- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE FAMILY.
CC -1- SIMILARITY: CONTAINS 1 PROTEIN KINASE-LIKE DOMAIN.
CC -----
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CC -----
DR EMBL; M26896; AAA41205.1; -
DR PIR; A33300; OYRTBR.
DR HSSP; Q02846; 1AML.
DR InterPro; IPR001828; ANP_receptor.
DR InterPro; IPR000719; Euk_Pkinase.
DR InterPro; IPR001054; G_cyclase.
DR InterPro; IPR001170; Ntpep_receptor.
DR Pfam; PF00069; Pkinase.1.
DR Pfam; PF00211; guanylate_cyc.1.
DR Pfam; PF01094; ANP_receptor.1.
DR PRINTS; PR00255; NARPEPTIDER.
DR ProDom; PD000001; Euk_Pkinase.1.
DR SMART; SM00044; CYC; 1.
DR PROSITE; PS00458; ANP_RECEPTORS; 1.
DR PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.
DR PROSITE; PS0125; GUANYLATE_CYCLASES_2; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Receptor; Transmembrane; Glycoprotein; Phosphorylation; Lyase;
KW cGMP synthesis; Signal.
FT CHAIN 1 22
FT SIGNAL 23 458
FT DOMAIN 23 458
FT TRANSMEM 459 478
FT DOMAIN 479 1047
FT DOMAIN 513 786
FT DOMAIN 861 991
FT DISULFID 75 101
BY SIMILARITY.

FT DISULFID 439 439 INTERCHAIN (PROBABLE).
FT DISULFID 448 448 INTERCHAIN (PROBABLE).
FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 35 35 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 349 349 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1047 AA; 117126 MW; 5062C49228C14A3 CRC64;
Query Match 12.8%; Score 460; DB 1; Length 1047;
Best Local Similarity 41.9%; Pred. No. 2; be-24;
Matches 113; Conservative 39; Mismatches 76; Indels 42; Gaps 6;
QY 411 DVLVIGEOARAD-----GLKRRGK-----LKATPEOA 439
DB 760 ELVILMERCAQADPTERPDRQIGFIRFRKKEGSIILNLLRMQYANNEKVEER 819
QY 440 HQALEEKRTVDLLCSIFCEVAQQLMGQVQAKFSVNTMLFSDIVGFTALCSQSP 499
DB 820 TQAVLEERKRAEALLYOILPHSVAEQLKRGFTVQAEAFDSVTIFYSDIVGFTALASBP 879
QY 500 LQVITMNLATYTRDQCGELDYKVKETIDGAYCVAGL-HKESDTAVQIALMALQME 558
DB 880 MQVVTLLNDLTCTFDALIDNFDYKVFETIGDAIVVSGLGRNGQRIAPETARALAL- 938
QY 559 LSEVMS-----PHGEPIKRIGLHSGSVFAGVGVKMPRYCIGNNVTLANFESCSV 612
DB 939 --DAVSSFRIHRH-DQLRRIRGVHGPACAGVGLKMPRYCLFGSTVMTASMEBSNG 995
QY 613 PKINVSPTTYRLKDCRGVFTPRSRREL 642
DB 996 ALKIVSSYTKDALDELGCQLELDGDEVEM 1025
RESULT 15
ANP_RAT STANDARD; PRT: 1057 AA.

AC P18910;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Atrial natriuretic peptide receptor A precursor (ANP-A) (ANPRA) (GC-A)
DE (Guanylate cyclase) (EC 4.6.1.2) (NPR-A) (Atrial natriuretic peptide A-type receptor).
GN NPR1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RX MEDLINE=69143770; PubMed=2563900;
RA Chinkers M., Garbers D.L., Chang M.S., Lowe D.G., Chin H., Goeddel D.V., Schulz S.;
RT "A membrane form of guanylate cyclase is an atrial natriuretic peptide receptor.";
RL Nature 338:78-83(1989).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91056089; PubMed=1978722;
RA Yamaguchi M., Rutledge J.J., Garbers D.L.;
RT "The primary structure of the rat guanylyl cyclase A/atrial natriuretic peptide receptor gene.";
RL J Biol. Chem. 265:20414-20420(1990).
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=91352095; PubMed=1679239;
RA Duda T., Gorczniak R.M., Sharma R.K.;
RT "Site-directed mutational analysis of a membrane guanylate cyclase cDNA reveals the atrial natriuretic factor signaling site.";

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OM protein - protein search, using sw model

Run on: June 27, 2003, 12:55:07 ; Search time 9.93048 Seconds

(without alignments)
2585.358 Million cell updates/sec

Title: US-09-762-767a-4

Perfect score: 3231
Sequence: 1 MGYVNALELVIRNGPE.....QVFLSRKNTGETTKODD 619

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3231	100.0	619	1	CYGL_HUMAN
2	3206	99.2	619	1	CYGL_BOVIN
3	3188	98.7	619	1	CYGL_RAT
4	987	30.5	682	1	CYGL_RAT
5	927	28.7	617	1	CYGL_HUMAN
6	916	28.4	730	1	CYGL_RAT
7	909.5	28.1	732	1	CYGL_HUMAN
8	793	24.5	690	1	CYGL_RAT
9	789.5	24.4	690	1	CYGL_HUMAN
10	770	22.8	691	1	CYGL_BOVIN
11	712	14.9	1061	1	CYGL_DROME
12	481.5	14.5	1057	1	ANPA_HUMAN
13	468	14.4	1057	1	ANPA_RAT
14	466	14.4	1057	1	ANPA_MOUSE
15	454.5	14.1	1047	1	ANPB_RAT
16	453.5	14.0	1047	1	ANPB_HUMAN
17	450.5	13.9	1047	1	ANPB_BOVIN
18	438.5	13.6	1110	1	CYGL_BOVIN
19	433.5	13.4	1108	1	CYGL_MOUSE
20	433	13.4	1109	1	CYGL_CANEA
21	428.5	13.3	1108	1	CYGL_RAT
22	425	13.2	1050	1	ANPB_ANGUA
23	424	13.1	1108	1	CYGL_HUMAN
24	422.5	13.1	1103	1	CYGL_HUMAN
25	420	13.0	1108	1	CYGL_RAT
26	419	13.0	1103	1	CYGL_BOVIN
27	415.5	12.9	1110	1	CYGL_RAT
28	410	12.7	1137	1	CYGL_CAEEL
29	409	12.7	433	1	KSCC_RAT
30	405.5	12.6	1073	1	HSEB_HUMAN
31	405	12.5	1073	1	HSEB_PIG
32	404	12.5	1072	1	HSEB_RAT
33	391	12.1	1125	1	CYGL_STRPT

34	389	12.0	1076	1	HSEB_CAVPO
35	345.5	10.7	443	1	CYAL_MYCTU
36	309.5	9.6	1134	1	CYAL_BOVIN
37	308.5	9.5	1248	1	CYAL_RAT
38	302.5	9.4	1251	1	CYAL_HUMAN
39	302.5	9.4	1305	1	CYAL_XENLA
40	301.5	9.3	839	1	CYAL_HUMAN
41	301.5	9.3	1249	1	CYAL_MOUSE
42	300.5	9.3	2248	1	CYAL_DROME
43	299	9.3	858	1	CYAL_DICDI
44	293	9.1	1144	1	CYAL_HUMAN
45	292.5	9.1	1334	1	CYAL_CHICK

ALIGNMENTS

RESULT 1
ID CYGL_HUMAN STANDARD: PRT; 619 AA.
AC 002153;
DT 01-JUL-1993 (Rel. 26, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Guanylate cyclase soluble, beta-1 chain (EC 4.6.1.2) (CCS-beta-1)
DE (Soluble guanylate cyclase small subunit) (CCS-beta-3).
GN GUCY1B1 OR GUCY1B3 OR GUC1B3 OR GUCS83.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RX MEDLINE=92316204; PubMed=1352257;
RA Giulii G., Scholl U., Bulle F., Gueilleen G.;
RT Molecular cloning of the cDNAs coding for the two subunits of
RT soluble guanylyl cyclase from human brain.";
RL FEBS Lett. 304:83-88(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM HSCG-2).
RC TISSUE-Kidney;
RA Gansemaus Y., Brouckaert P., Fiers W.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RC SEQUENCE OF 337-545, AND ALTERNATIVE SPLICING.
RX MEDLINE=92008652; PubMed=1680753;
RA Chhajlani V., Friendberg P.-A., Ahlner J., Axelsson K.L.,
RT Wikberg J.E.S.;
RT "Heterogeneity in human soluble guanylate cyclase due to alternative
RT splicing.";
RL FEBS Lett. 290:157-158(1991).
CC -1- CATALYTIC ACTIVITY: GTP -> 3',5'-cyclic GMP + diphosphate.
CC -1- ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE OF
CC MAGNESIUM OR MANGANESE IONS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; HSCG-1 (SHOWN HERE) AND HSCG-2;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES: SOLUBLE
CC FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
CC -1- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
CC FAMILY.
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CC or send an email to license@isb-sib.ch).

DR EMBL: X66533; CAA47144.1; -
 DR EMBL: AF020340; AAB94877.1; -
 DR PIR: S23097; S23097.
 DR HSSP: P16068; IAWN.
 DR Genew: HGNC:4687; GUCY1B3.
 DR MIM: 139397; -
 DR InterPro: IPR001054; G_cyclase.
 DR Pfam: PF00211; guanylate_cyc; 1.
 DR SMART: SM00044; CYC; 1.
 DR PROSITE: PS00452; GUANYLATE_CYCLASES_1; 1.
 DR PROSITE: PS0125; GUANYLATE_CYCLASES_2; 1.
 DR Lysase: CGMP synthesis; Alternative splicing.
 KM DOMAIN 421 554 GUANYLATE CYCLASE.
 FT VARSPLIC 393 425 MISSING (IN ISOFORM HSGC-2).
 SQ SEQUENCE 619 AA; 70514 MW; 231E4E60DE02A1 CRC64;

Query Match 100.0%; Score 3231; DB 1; Length 619;
 Best Local Similarity 100.0%; Pred. No. 2e-215;
 Matches 619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYGFVNAHELVIRNYGPEWEDIKKEAQLDEGQFLVRIYDSTKYDLVAASKVLN 60
 DB 1 MYGFVNAHELVIRNYGPEWEDIKKEAQLDEGQFLVRIYDSTKYDLVAASKVLN 60
 QY 61 LNAGEILQMFGRKMFVFCQESGYTLIRVLSNREFLQNDALDHLATITPGMRAPSF 120
 DB 61 LNAGEILQMFGRKMFVFCQESGYTLIRVLSNREFLQNDALDHLATITPGMRAPSF 120
 QY 121 RCTDAERKGLILHYSEREGLODIYIGITVAQIHGTEIDMKYIQORNECDHTQFL 180
 DB 121 RCTDAERKGLILHYSEREGLODIYIGITVAQIHGTEIDMKYIQORNECDHTQFL 180
 QY 122 RCTDAERKGLILHYSEREGLODIYIGITVAQIHGTEIDMKYIQORNECDHTQFL 180
 DB 122 RCTDAERKGLILHYSEREGLODIYIGITVAQIHGTEIDMKYIQORNECDHTQFL 180
 QY 181 IEKESKEDEYEDLDREENGQESRISPTFCAPPHIIFDRDLVTVQCGNAIYRYL 240
 DB 181 IEKESKEDEYEDLDREENGQESRISPTFCAPPHIIFDRDLVTVQCGNAIYRYL 240
 QY 181 IEKESKEDEYEDLDREENGQESRISPTFCAPPHIIFDRDLVTVQCGNAIYRYL 240
 DB 181 IEKESKEDEYEDLDREENGQESRISPTFCAPPHIIFDRDLVTVQCGNAIYRYL 240
 QY 241 POLQPCNSLISVFSYVRPHIDISPHGISHTNVTVLRSKGLDVEKLEDEDELGTGE 300
 DB 241 POLQPCNSLISVFSYVRPHIDISPHGISHTNVTVLRSKGLDVEKLEDEDELGTGE 300
 QY 241 POLQPCNSLISVFSYVRPHIDISPHGISHTNVTVLRSKGLDVEKLEDEDELGTGE 300
 DB 241 POLQPCNSLISVFSYVRPHIDISPHGISHTNVTVLRSKGLDVEKLEDEDELGTGE 300
 QY 301 ISCLRLKGMITLPEADSLIFLCSPSVMNLDLTRKGLYSDIPLHADRDLVLGQPR 360
 DB 301 ISCLRLKGMITLPEADSLIFLCSPSVMNLDLTRKGLYSDIPLHADRDLVLGQPR 360
 QY 301 ISCLRLKGMITLPEADSLIFLCSPSVMNLDLTRKGLYSDIPLHADRDLVLGQPR 360
 DB 301 ISCLRLKGMITLPEADSLIFLCSPSVMNLDLTRKGLYSDIPLHADRDLVLGQPR 360
 QY 361 EEKRLQELIELDRLQLTLRALDEKKTDTLLSVLPSSVANELRKRPPAKRYDNV 420
 DB 361 EEKRLQELIELDRLQLTLRALDEKKTDTLLSVLPSSVANELRKRPPAKRYDNV 420
 QY 361 EEKRLQELIELDRLQLTLRALDEKKTDTLLSVLPSSVANELRKRPPAKRYDNV 420
 DB 361 EEKRLQELIELDRLQLTLRALDEKKTDTLLSVLPSSVANELRKRPPAKRYDNV 420
 QY 421 TILFSGIVGFNAFCSHASGEGAMKIVNLNDLYRFDLTDSRKMPFYKYEYGDKN 480
 DB 421 TILFSGIVGFNAFCSHASGEGAMKIVNLNDLYRFDLTDSRKMPFYKYEYGDKN 480
 QY 421 TILFSGIVGFNAFCSHASGEGAMKIVNLNDLYRFDLTDSRKMPFYKYEYGDKN 480
 DB 421 TILFSGIVGFNAFCSHASGEGAMKIVNLNDLYRFDLTDSRKMPFYKYEYGDKN 480
 QY 481 TVSGIPEPCIHARSICHLALDMMETAGOVQVDSGVOITIGIHGEVTVGVIGORMPY 540
 DB 481 TVSGIPEPCIHARSICHLALDMMETAGOVQVDSGVOITIGIHGEVTVGVIGORMPY 540
 QY 481 TVSGIPEPCIHARSICHLALDMMETAGOVQVDSGVOITIGIHGEVTVGVIGORMPY 540
 DB 481 TVSGIPEPCIHARSICHLALDMMETAGOVQVDSGVOITIGIHGEVTVGVIGORMPY 540
 QY 541 CLFGNTVNTSRFTTGEKGINVSEYTYRCLMSPNSDPQPHLEHGRVPSKGRKPEMQ 600
 DB 541 CLFGNTVNTSRFTTGEKGINVSEYTYRCLMSPNSDPQPHLEHGRVPSKGRKPEMQ 600
 QY 541 CLFGNTVNTSRFTTGEKGINVSEYTYRCLMSPNSDPQPHLEHGRVPSKGRKPEMQ 600
 DB 541 CLFGNTVNTSRFTTGEKGINVSEYTYRCLMSPNSDPQPHLEHGRVPSKGRKPEMQ 600
 QY 601 VWFELSKNTGTEETKODDD 619
 DB 601 VWFELSKNTGTEETKODDD 619
 QY 601 VWFELSKNTGTEETKODDD 619
 DB 601 VWFELSKNTGTEETKODDD 619

RESULT 2

CYCL_BOVIN STANDARD; PRT; 619 AA.

AC P16068; 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Guanylate cyclase soluble, beta-1 chain (EC 4.6.1.2) (GCS-beta-1)

DE (Soluble guanylate cyclase small subunit).
 GN GUCY1B1 OR GUCY1B3 OR GUCY1B3.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Lung;
 RX MEDLINE=89031214; PubMed=2903071;
 RA Koesling D., Herz J., Gausepohl H., Niroomand F., Hirsch K.-D.,
 Wueisch A., Boelme E., Schultz G., Frank R.;
 RT "The primary structure of the 70 kDa subunit of bovine soluble
 guanylate cyclase."
 RL FEBS Lett. 239:29-34 (1988).
 RN [2]
 RP 3D-STRUCTURE MODELING OF 412-572.
 RX MEDLINE=98054247; PubMed=9391039;
 RA Liu Y., Ruoho A.E., Rao V.D., Hurley J.H.;
 RT "Catalytic mechanism of the adenylyl and guanylyl cyclases: modeling
 and mutational analysis."
 RL Proc. Natl. Acad. Sci. U.S.A. 94:13414-13419 (1997).
 CC -1- CATALYTIC ACTIVITY: GTP -> 3',5'-cyclic GMP + diphosphate.
 CC -1- ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE OF
 MAGNESIUM OR MANGANESE IONS.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: LUNG AND BRAIN.
 CC -1- MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES: SOLUBLE
 FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
 CC -1- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
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 or send an email to license@isb-sib.ch).

DR EMBL: Y00770; CAA68739.1; -
 DR PIR: S01653; OYB070.
 DR PDB: IAWN; 28-JAN-98.
 DR InterPro: IPR001054; G_cyclase.
 DR Pfam: PF00211; guanylate_cyc; 1.
 DR SMART: SM00044; CYC; 1.
 DR PROSITE: PS00452; GUANYLATE_CYCLASES_1; 1.
 DR PROSITE: PS0125; GUANYLATE_CYCLASES_2; 1.
 DR Lysase: CGMP synthesis; 3D-structure.
 KM DOMAIN 421 554 GUANYLATE CYCLASE.
 FT SEQUENCE 619 AA; 70502 MW; 8EFB14952B80F344 CRC64;

Query Match 99.2%; Score 3206; DB 1; Length 619;
 Best Local Similarity 99.0%; Pred. No. 1e-213;
 Matches 613; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 MYGFVNAHELVIRNYGPEWEDIKKEAQLDEGQFLVRIYDSTKYDLVAASKVLN 60
 DB 1 MYGFVNAHELVIRNYGPEWEDIKKEAQLDEGQFLVRIYDSTKYDLVAASKVLN 60
 QY 61 LNAGEILQMFGRKMFVFCQESGYTLIRVLSNREFLQNDALDHLATITPGMRAPSF 120
 DB 61 LNAGEILQMFGRKMFVFCQESGYTLIRVLSNREFLQNDALDHLATITPGMRAPSF 120
 QY 121 RCTDAERKGLILHYSEREGLODIYIGITVAQIHGTEIDMKYIQORNECDHTQFL 180
 DB 121 RCTDAERKGLILHYSEREGLODIYIGITVAQIHGTEIDMKYIQORNECDHTQFL 180
 QY 121 RCTDAERKGLILHYSEREGLODIYIGITVAQIHGTEIDMKYIQORNECDHTQFL 180
 DB 121 RCTDAERKGLILHYSEREGLODIYIGITVAQIHGTEIDMKYIQORNECDHTQFL 180
 QY 181 IEKESKEDEYEDLDREENGQESRISPTFCAPPHIIFDRDLVTVQCGNAIYRYL 240
 DB 181 IEKESKEDEYEDLDREENGQESRISPTFCAPPHIIFDRDLVTVQCGNAIYRYL 240
 QY 181 IEKESKEDEYEDLDREENGQESRISPTFCAPPHIIFDRDLVTVQCGNAIYRYL 240
 DB 181 IEKESKEDEYEDLDREENGQESRISPTFCAPPHIIFDRDLVTVQCGNAIYRYL 240


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OY 241 POLPGNCSLSVSVLPVRPHIDISFHGILSHINTVFLRSKRGLLDVEKLECEDELGTGE 300
DB 241 POLPGNCSLSVSVLPVRPHIDISFHGILSHINTVFLRSKRGLLDVEKLECEDELGTGE 300
OY 301 ISCLRLKGMITLPRADSLIFLCSPSVNMDDLTRRGYLSIPPLHADRDLVLLGEOR 360
DB 301 ISCLRLKGMITLPRADSLIFLCSPSVNMDDLTRRGYLSIPPLHADRDLVLLGEOR 360
OY 361 EBYKLTQELIETDLRLQTLRALDEKKKTDPLTSVPPSVANELRHRKRPVPAKRYDNV 420
DB 361 EBYKLTQELIETDLRLQTLRALDEKKKTDPLTSVPPSVANELRHRKRPVPAKRYDNV 420
OY 421 TILFSGIVGFNAFCSKHAASGEGAMKIVNLNDLYTRFDPLTDSRKNPFYKVEYGDXYM 480
DB 421 TILFSGIVGFNAFCSKHAASGEGAMKIVNLNDLYTRFDPLTDSRKNPFYKVEYGDXYM 480
OY 481 TVSGLPFPCIHARSICHLADMMELIAGOVYDGSVOITIGIHGEVYTVYIGORMPRY 540
DB 481 TVSGLPFPCIHARSICHLADMMELIAGOVYDGSVOITIGIHGEVYTVYIGORMPRY 540
OY 541 CLFGNTVNLTSRTETTGEGKINVSERYTYRCIMSPENDPOPHLEHRGVSMSKGRKPEMQ 600
DB 541 CLFGNTVNLTSRTETTGEGKINVSERYTYRCIMSPENDPOPHLEHRGVSMSKGRKPEMQ 600
OY 601 VWFLSRKNKTGTEETKODDD 619
DB 601 VWFLSRKNKTGTEETKODDD 619

RESULT 3
CYG1_RAT STANDARD: PRT: 619 AA.
AC P20595;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Guanylate cyclase soluble, beta-1 chain (EC 4.6.1.2) (GCS-beta-1)
GN GUCY1B1 OR GUCY1B3 OR GUC1B3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus;
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=89087429; PubMed=2905128;
RA Nakane M., Sahel S., Kuno T., Ishii K., Murad F.;
RT "Molecular cloning of a cDNA coding for 70 kilodalton subunit of
RT soluble guanylate cyclase from rat lung.";
RL Biochem. Biophys. Res. Commun. 157:1139-1147(1988).
CC -1- CATALYTIC ACTIVITY: GTP -> 3',5'-cyclic GMP + diphosphate.
CC -1- ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE OF
CC MAGNESIUM OR MANGANESE IONS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: LONG AND BRAIN.
CC -1- MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES: SOLUBLE
CC FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
CC -1- SIMILARITY: BELONGS TO ADENYLAT CYCLASE CLASS-4/GUANYLYL CYCLASE
CC FAMILY.
CC -----
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CC or send an email to license@isb-sdb.ch).
CC -----
CC EMBL, M22562; AAA41204.1; .
CC DR PIR: A31871; OYRBL.
CC HSP: P16068; 1AWN.

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DR InterPro: IPR001054; G_cyclase.
DR Pfam: PF00211; guanylate_cyc; 1.
DR SMART: SM00044; CYC; 1.
DR PROSITE: PS00452; GUANYLATE_CYCLASES_1; 1.
DR PROSITE: PS00125; GUANYLATE_CYCLASES_2; 1.
KW Lyase; GMP synthesis.
FT DOMAIN 421 554
SQ SEQUENCE 619 AA; 70477 MW; BCC9850DE4504226 CRC64;

Query Match 98.7%; Score 3188; DB 1; Length 619;
Best Local Similarity 98.5%; Pred. No. 1,8e-212;
Matches 610; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 1 MTGFVNHAEELVINYNGEVEDIKKEAQDDEGOFVRIIYDSDKTYDLVAASKVYN 60
DB 1 MTGFVNHAEELVINYNGEVEDIKKEAQDDEGOFVRIIYDSDKTYDLVAASKVYN 60
OY 61 INAGELIOMFGMFVFCOESGYDTILRVLSNVREFLQNLALHDHLATIPGMRAPSF 120
DB 61 INAGELIOMFGMFVFCOESGYDTILRVLSNVREFLQNLALHDHLATIPGMRAPSF 120
OY 121 RCTDAEKGGLILHYSEREGIADIVIGIKTVAAQIHGTETDMKVIOQRNECHTOPL 180
DB 121 RCTDAEKGGLILHYSEREGIADIVIGIKTVAAQIHGTETDMKVIOQRNECHTOPL 180
OY 181 IEKESKEDEYEDLDREENGTOESRISPYTFCKAFPHIIFDRDLVYTOGNAIYRYL 240
DB 181 IEKESKEDEYEDLDREENGTOESRISPYTFCKAFPHIIFDRDLVYTOGNAIYRYL 240
OY 241 POLPGNCSLSVSVLPVRPHIDISFHGILSHINTVFLRSKRGLLDVEKLECEDELGTGE 300
DB 241 POLPGNCSLSVSVLPVRPHIDISFHGILSHINTVFLRSKRGLLDVEKLECEDELGTGE 300
OY 301 ISCLRLKGMITLPRADSLIFLCSPSVNMDDLTRRGYLSIPPLHADRDLVLLGEOR 360
DB 301 ISCLRLKGMITLPRADSLIFLCSPSVNMDDLTRRGYLSIPPLHADRDLVLLGEOR 360
OY 361 EBYKLTQELIETDLRLQTLRALDEKKKTDPLTSVPPSVANELRHRKRPVPAKRYDNV 420
DB 361 EBYKLTQELIETDLRLQTLRALDEKKKTDPLTSVPPSVANELRHRKRPVPAKRYDNV 420
OY 421 TILFSGIVGFNAFCSKHAASGEGAMKIVNLNDLYTRFDPLTDSRKNPFYKVEYGDXYM 480
DB 421 TILFSGIVGFNAFCSKHAASGEGAMKIVNLNDLYTRFDPLTDSRKNPFYKVEYGDXYM 480
OY 481 TVSGLPFPCIHARSICHLADMMELIAGOVYDGSVOITIGIHGEVYTVYIGORMPRY 540
DB 481 TVSGLPFPCIHARSICHLADMMELIAGOVYDGSVOITIGIHGEVYTVYIGORMPRY 540
OY 541 CLFGNTVNLTSRTETTGEGKINVSERYTYRCIMSPENDPOPHLEHRGVSMSKGRKPEMQ 600
DB 541 CLFGNTVNLTSRTETTGEGKINVSERYTYRCIMSPENDPOPHLEHRGVSMSKGRKPEMQ 600
OY 601 VWFLSRKNKTGTEETKODDD 619
DB 601 VWFLSRKNKTGTEETKODDD 619

RESULT 4
CYG2_RAT STANDARD: PRT: 682 AA.
AC P22717;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Guanylate cyclase soluble, beta-2 chain (EC 4.6.1.2) (GCS-beta-2).
GN GUCY1B2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus;
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE-Kidney;
RX MEDLINE-91105012; PubMed-1980215;
RA Yuen P.S.T., Potter L.R., Garbers D.L.;
RT "A new form of guanylyl cyclase is preferentially expressed in rat kidney."
RL Biochemistry 29:10872-10878(1990).
CC -1- CATALYTIC ACTIVITY: GTP -> 3',5'-cyclic GMP + diphosphate.
CC -1- ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE OF MAGNESIUM OR MANGANESE IONS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: KIDNEY AND LIVER.
CC -1- MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES: SOLUBLE FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
CC -1- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE FAMILY.
CC -----
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CC -----
DR EMBL; M57507; AAA41207.1; -
DR PIR; A36228; OYRTB2.
DR HSSP; P19687; 1AMN.
DR InterPro; IPR001054; G_cyclase.
DR InterPro; IPR001230; Prenyl_site.
DR Pfam; PF00211; guanylate_cyc; 1.
DR SMART; SM00044; CYCC; 1.
DR PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.
DR PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
DR Lyase; CGMP synthesis.
DR FT DOMAIN 408 536 GUANYLATE CYCLASE.
DR SQ SEQUENCE 682 AA; 76196 MM; 98C173C1A1CC7715 CRC64;
Query Match 30.5%; Score 987; DB 1; Length 682;
Best Local Similarity 36.9%; Pred. No. 1.4e-60;
Matches 225; Conservative 104; Mismatches 195; Indels 86; Gaps 12;
QY 66 ILDMGKMFVPCOESGYDILIRVSGNVEFLQNDALDHLATIPGRAPSFCTDA 125
DB 4 ILDFGEYFKFKMSGYDMLKRLTGSLTEFLNDALSYALSYQENMABSFREEG 63
QY 126 EKSGGLIATYSEREGADIVIGIKYVAQOIHGTEIDMKVIOQRNEC-----DHTQF 179
DB 64 ADG-AMLIHYSDRHGCHIVPGIIEAVAKDFPTDVAMSLDM-NEVERTGKREHYF 121
QY 180 LIEBKESKE-----EDFYED----- 194
DB 122 LVVQAKARQIRGAKASRPGSEDSQADQALQGLTLNKKERYINIPVCGEKSHSTAVRA 181
QY 195 -----LDREENTQGSRTISPYTFCAFPHTIEDDVLVTOGGMATYRPLQ 245
DB 182 SVLFGGLDQTPVYPERLWEEVEVCAFPPIHYFDALRKQAGVNIQKVPILTF 241
QY 246 GNCGLSVGLVPHRIDISFHLISHTVFLVSKGLDVEKCEDELTGETEISCLR 305
DB 242 QKRALDEYFIIHPVTFNFISSICKFINSQFVLKTRKEMPKAR-----KSGPMK 292
QY 306 LKQOMIYLPADSIPLCSPSVANLDDLTRRGLYLSDIPLDATRDILVLLGEQFREERYKL 365
DB 293 LRCQIMWESLRQIMFICSPNVSRIQLEESKMLSDIADPHDTTRDILINQOLAMEL 352
QY 366 TQLEILITDQLTLRLDEKKTDTLLYSVLPSPVANLRRKRPAPARYDNVTLFS 425
DB 353 SCQLERKKEELRYLSNHLATEKKRTETLLYAMLPEHYANOLKGRKVAAGEFECTILFS 412
QY 426 GIVGFNAFCSKHAGSEGAMIVNLNDLYTRPDTLFSRKRNPFYKVEYWGDKYMTVSGL 485
DB 413 DVTFTNLC---AAFC-PIQIYVNMNLSKFKDRILTSVHD---YKVEYIGDAIMVVGCV 465

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QY 486 PEPCHHRSICHLALDMEIAGVQ--VDGESVQITIGITGEVTVYIGOMPRYCLF 543
DB 466 PVPESHAQVAVNPFALGMRISAKENVMPVGEPIQIVGHTSPVLAVGVDGMDMRCPLF 525
QY 544 GNYVNLTSKRTETGEEKKIVSEYTRVCLMSPENSDQFHLERHGPVSMGKKEPMQVWF 603
DB 526 GDTYVNLNRSRSHQLPSKVLSPFAHRAL-----KNNGFEIVRGEIEVGKGR-MTTYF 579
QY 604 LSRKNTGEE 613
DB 580 LIQUNATED 589
RESULT 5
CYG2 HUMAN
ID CYG2_HUMAN STANDARD; PRT; 617 AA.
AC 075343; 09NZ64;
DT 15-JUL-1999 (Rel. 38, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Guanylate cyclase soluble, beta-2 chain (EC 4.6.1.2) (GCS-beta-2).
GN GUCY1B2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_Taxid=9606;
RN 1;
RP SEQUENCE FROM N.A., AND REVISION TO 175.
RC TISSUE-Kidney;
RX MEDLINE-20241821; PubMed-10777682;
RA Behrends S., Vense K.;
RT "The beta(2) subunit of soluble guanylyl cyclase contains a human-specific frameshift and is expressed in gastric carcinoma."
RL Biochem. Biophys. Res. Commun. 271:64-69(2000).
RN 12;
RP SEQUENCE OF 95-257 FROM N.A.
RC TISSUE-Heart;
RX MEDLINE-99107820; PubMed-9889008;
RA Behrends S., Kazmierczak B., Steenpa A., Knauf B., Bullerdiek J., Scholz H., Elberg H.;
RT "Assignment of GUCY1B2, the gene coding for the beta2 subunit of human guanylyl cyclase to chromosomal band 13q14.3 between markers D13S168 and D13S155."
RL Genomics 55:126-127(1999).
CC -1- CATALYTIC ACTIVITY: GTP -> 3',5'-cyclic GMP + diphosphate.
CC -1- ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE OF MAGNESIUM OR MANGANESE IONS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES: SOLUBLE FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
CC -1- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE FAMILY.
CC -----
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CC -----
DR EMBL; AF038499; AAD09440.2; -
DR EMBL; AF218383; AAF66105.1; -
DR HSSP; P19687; 1AMN.
DR Genew; HGNC:4686; GUCY1B2.
DR MIM; 603695; -
DR InterPro; IPR001054; G_cyclase.
DR Pfam; PF00211; guanylate_cyc; 1.
DR SMART; SM00044; CYCC; 1.
DR PROSITE; PS00452; GUANYLATE_CYCLASES_1; FALSE_NEG.
DR PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.

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LYase: cGMP synthesis.
 FT DOMAIN 391 519 GUANYLATE CYCLASE.
 SQ SEQUENCE 617 AA: 70367 MW: 186C9655CAB9A5E3E CRC64;

Query Match 28.7%; Score 927; DB 1; Length 617;
 Best Local Similarity 36.6%; Pred. No. 1.6e-56;
 Matches 218; Conservative 96; Mismatches 195; Indels 86; Gaps 11;

QY 81 SGYDILRLVLSNVRELFQNDLADHDLATVYPGMRKPSFCTDAERKGLILHYSSERE 140
 DB 2 SGYDRLRLGNGLEMEFLENLADLSYALSTQENNAFSEVERGADGK-MELHYSSDRS 60
 QY 141 GLQDVLIGIKTVAAQINGTEIDMKVIOQRNEC-----DITQFLIEKES----- 186
 DB 61 GLCHTIPGIIIEAVANDPFDVIDIILDM-NEEVERTEGKEHVVFLVQKARRKKRKTTP 119
 QY 187 -----KEEDFYED-----LDREFE 200
 DB 120 KRLDSQGMERDQELQAFLKMKREKYLNSACPYKSHMDVYRSIVMGKGLHANTFEP 179
 QY 201 NGTQESRISPYTECKAPPHIIFEDRLVVTQCGNAIYRVLPOLQPGNCSLVSFLVRPH 260
 DB 180 IYPERLMTIEKTEFCNAFPFHIVFDESLQVKARVNIOKYPGLQIQONQIDREYFSIIHQ 239
 QY 261 IDISFHGLSHNTVFLVRSKRGGLDVERKECEDELGTETICSLRKQMTILPEADSL 320
 DB 240 VTFENFSIRRFINSQFVLKTRREMPV-----AMQSRTTLKIQGGMIMESMWCYV 290
 QY 321 FLCSPSVNNLDLDFRGLYLSIDPLHDAATRLVLDGEOPREYKTLQOELEITLDRLOLT 380
 DB 291 YLCSKRLSLQLEELNHLNLSIAPNDTTRDILINQRLAIEISNOLERKEELQVLS 350
 QY 381 RALEDEKKTDTLLYSVLPSPVANELRHRKRPVPAKRYDNTLIFSGIVGFNAFCSKASG 440
 DB 351 KHLAEKKEKTELLTAMLPKHVAANOLREKKAAGEFSCITLIFSDVYFTNICTACE-- 408
 QY 441 EGAMKIVMLNDLYRFDLIDSRKNRPYKVEYTGDKMYSGLEPDIHARSCHLA 500
 DB 409 --PIQIVVNLMSKSPKFDLSVHA--YKVEYTGDAVGVGVPPVIGNAQRANPA 463
 QY 501 LDMELIAGOV--QVDSVOITIGIHTGEVTVVIGORMPRYCLFGNVNLISRTETGE 558
 DB 464 LGMRSAREVTPVGEPIQLRVGHTGVLADYVGDKMRPCLGDTYNTASRMESHSL 523
 QY 559 KGIIVSEYTYRCLMSPENSDFPHLEHRGPVSMKKEKPEQVWELSKNRTGEE 613
 DB 524 PKVHLSFAYRAL-----KNOGFRIIEGELIEVGKGR-MTYVFLIQMLNATED 572

RESULT 6
 CYG4_RAT
 ID CYG4_RAT STANDARD; PRT; 730 AA.
 AC O9WV14;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Guanylate cyclase soluble, alpha-2 chain (EC 4.6.1.2) (GCS-alpha-2).
 GN GUCY1A2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mistar Kyoto; TISSUE=Aorta;
 RX MEDLINE=20571097; PubMed=11121588;
 RA Koglin M., Behrends S.;
 RT "Cloning and functional expression of the rat alpha(2) subunit of
 soluble guanylyl cyclase."
 RL Biochim. Biophys. Acta 1494:286-289(2000).
 CC -1- FUNCTION: HAS GUANYLYL CYCLASE ON BINDING TO THE BETA-1 SUBUNIT.
 CC -1- CATALYTIC ACTIVITY: GTP -> 3',5'-cyclic GMP + diphosphate.
 CC -1- ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE OF

CC MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES: SOLUBLE
 CC FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
 CC -1- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS 4/GUANYLYL CYCLASE
 CC FAMILY.
 CC -----
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 CC -----

DR EMBL: AF109963; AAD42949.2; .
 DR HSSP: P19687; IAWN.
 DR InterPro: IPR001054; G_cyclase.
 DR Pfam: PF00211; guanylate_cyc; 1.
 DR SMART: SM00044; CYCC; 1.
 DR PROSITE: PS00452; GUANYLATE_CYCLASES_1; 1.
 DR PROSITE: PS01025; GUANYLATE_CYCLASES_2; 1.
 KM LYase: cGMP synthesis; Multigene family.
 FT DOMAIN 319 646 GUANYLATE CYCLASE.
 FT DOMAIN 50 72 ALA-RICH.
 FT DOMAIN 64 72 POLY-ALA.
 SQ SEQUENCE 730 AA: 81786 MW: 880790BFF81FB8F9 CRC64;

Query Match 28.4%; Score 916; DB 1; Length 730;
 Best Local Similarity 38.0%; Pred. No. 1.2e-55;
 Matches 210; Conservative 116; Mismatches 167; Indels 60; Gaps 16;

QY 51 LVAASKVNLNLAAGELIOMFGKMFEEVCESGDTLIRVGSNVRELFQNDLADHDLAT 110
 DB 152 ILRCNTANVGLKFGELQERFGEFFKICDEN-ERLRAVAGSLQDFPFGDALLHIRT 210
 QY 111 IV--PGMRPSFCTDAERKGLILHYSSEREGLDVIIGIKTVAAQIHGTEIDMKYI 167
 DB 211 SFGKQATLSPSFLCKELPEGT-LKLHYRPHHTVGFAMIGMKAKGRIRYHLNVEVDI 269
 QY 168 QGR-----NECDHTQFLIEKESKEDEYDDDRFENGQ-----ERISPYTF 213
 DB 270 ENKFCSDGSTPSNISC--LTFLIKCECTQ-----ITKNIPQGSQIPLDRLISINF 321
 QY 214 CKAFFHIFEDRLVVTQCGNAIYRVLPOLQPGNCSL--SVFSVLRPHIDISFGITS 270
 DB 322 CRTFPFHLMEFDPNMVVLQLEGRLK---QLRCNHNVLKFEDECFEIVSRVNAETFRVLL 378
 QY 271 HINTVFLNSKRGGLDVERKECEDELGT--EISCLRLKQMTILPEADSLIFLCSPSYV 328
 DB 379 RLSTPEVIRTK-----PEASGTDNEDKVMKIGOMIHVESNALIFLGSPVD 426
 QY 329 NIDDLRLRLGLYLSIDPLHDAATRLVLDGEOPREYKTLQOELEITLDRLOLTALDEK 388
 DB 427 KIDELIGRGLHLSIDPIHDATRVILLVGDARAKDILKRMDLKATLLETQALDEERK 486
 QY 389 KFDVTLISVLPSPVANELRHRKRPVPAKRYDNTLIFSGIVGFNAFCSKASGAKIYV 448
 DB 487 KAYDILKSLFPGVAAQIQMQROOVAKRKDDVYMLFSDVIGFALTAQCT---PQGVIS 542
 QY 449 LNLDTYRFDTLIDSRKNRP--YKVEYTGDKMYVSGLEPDIHARSCHLALDMMEL 506
 DB 543 MLNELYTRFD-----HQCGFLDIYKVEYTGDAVGVGVPPVIGNAQRANPA 597
 QY 507 AGGVQV--DGEVQITIGIHTGEVTVVIGORMPRYCLFGNVNLISRTETGKGLINS 565
 DB 598 SEEVLPDGRPIQMRGISHSGVLAAGVGRMPRYCLFGNVNLISRTETGKGLINS 657
 QY 566 EYVRLMSPENS 578
 DB 658 PTTYQ-LLRKEDS 669

RESULT 7	CYG4_HUMAN	STANDARD:	PRF:	732 AA.
AC	P33402.			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Guanylate cyclase soluble, alpha-2 chain (EC 4.6.1.2) (GCS-alpha-2).			
GN	GUCY1A2 OR GUC1A2 OR GUCSA2.			
OS	Homo sapiens (Human).			
OC	Eumetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RA	Medline			
RA	Hattnack C., Wedel B., Koesling D., Malkevič J., Boehme E.,			
RT	"Molecular cloning and expression of a new alpha-subunit of soluble			
RT	guanylyl cyclase. Interchangeability of the alpha-subunits of the			
RT	enzyme."			
RL	FEBS Lett. 292:217-222(1991).			
RL	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA 2-1).			
RP	MEDLINE=95403342; PubMed=7673142;			
RX	Behrends S., Hattnack C., Schultz G., Koesling D.;			
RA	"A variant of the alpha 2 subunit of soluble guanylyl cyclase			
RT	contains an insert homologous to a region within adenylyl cyclases			
RT	and functions as a dominant negative protein.";			
RT	J. Biol. Chem. 270:21109-21113(1995).			
CC	-1- FUNCTION: HAS GUANYLYL CYCLASE ON BINDING TO THE BETA-1 SUBUNIT.			
CC	THE ALTERNATIVE SPLICED ISOFORM, ALPHA-2-1, ACTS AS A NEGATIVE			
CC	REGULATOR OF GUANYLYL CYCLASE ACTIVITY AS IT FORMS NON-FUNCTIONAL			
CC	HETERODIMERS WITH THE BETA SUBUNTS.			
CC	-1- CATALYTIC ACTIVITY: GTP -> 3',5'-cyclic GMP + diphosphate.			
CC	-1- ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE OF			
CC	MAGNESIUM OR MANGANESE IONS.			
CC	-1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.			
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic.			
CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ALPHA-2 (SHOWN HERE) AND			
CC	ALPHA-2-1; ARE PRODUCED BY ALTERNATIVE SPLICING.			
CC	-1- TISSUE SPECIFICITY: ALPHA-2 ISOFORM IS EXPRESSED IN FETAL BRAIN,			
CC	LIVER, COLON, ENDOTHELUM AND TESTIS, WHILE THE ALPHA-2-1 FORM			
CC	IS EXPRESSED ONLY IN LIVER, COLON AND ENDOTHELUM.			
CC	-1- MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLYL CYCLASES: SOLUBLE			
CC	FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.			
CC	-1- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE			
CC	FAMILY.			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announcement/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; X63382; CAA44921.1; -			
DR	EMBL; Z50053; CAA90393.1; -			
DR	PIR; S18325, S18325.			
DR	HSSP; P19687; IAMN.			
DR	Genew; HGNC:4684; GUCY1A2.			
DR	MIM; 601244; -			
DR	InterPro; IPR001054; G_cyclase.			
DR	Pfam; PF00211; guanylate_cyc; 1.			
DR	SMART; SM00044; CYC; 1.			
DR	PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.			
DR	PROSITE; PS01025; GUANYLATE_CYCLASES_2; 1.			
KW	Lyase; cGMP synthesis; Multigene family; Alternative splicing.			
FT	DOMAIN 521 648			
FT	DOMAIN 51 76			
FT	DOMAIN 51 58			
FT	POLY-ALA.			

FT	VSAPSLIC	612	612	O -> OROSELEFPVSIQVDPDQHSSEIDGTEK (IN ISOPORN ALPHA 2-1)
SO	SEQUENCE	732 AA;	81749 MM;	79465A7D3FE52DB7 CRC64;
	Query Match	28.1%;	Score 909.5;	DB 1; Length 732;
	Best Local Similarity	37.7%;	Pred. No. 3,3e-55;	
	Matches 208;	Conservative 111;	Mismatches 175;	Indels 57; Gaps 14
QY	51	LVAASAVYLNANGELQFQKMFYFQOESSYDILILAVGSSNNREFQINDALHDHLAT	110	
DB	154	ILQCTANILGLKFEETQKRFESEFNQICHEN-ERVLRAVGGLQADDFNGFDALLEHRT	212	
QY	111	IV---PGMKRSPRCTDAEKGKGLIHYSEEGQDIIYICITVYAAQIHGTEIDKVI	167	
DB	213	SPFKQATLSPSPSLCKELPEGT-LMHLFPHPHIYVGMAGMIMAKAKKIY--RLDVEYE	269	
QY	168	QQRNE-----CDHTQFLIEKSKEDFEDLDRENGTOBSRISPYTCKAF	217	
DB	270	QVANERKICSDVSNPGNSCLTFELI--KECENTNINIKMLPOSTQVPAIDLRIINTFCRAF	327	
QY	218	PFHIFDRDLVYQCGNATIRVILPOLQPCNSLSV-----FSIVRPHIDISPHGLISH	271	
DB	328	PHILMDDPSNIVQLQGBGRKQD-----RCDTHAVLKFECCFELVSPKVNATERVILR	381	
QY	272	INTFVPLRSKGLLDVEKLECEDELTGTE--ISCLRKGOMIYLPREADSILFLCSPSVAN	339	
DB	382	LSPPFYLRFK-----PEASGSENNKRVKVEVKGQMIHPESNSILFLGSPCVDK	429	
QY	330	LDLTFRRGGLYSDIPILHDATRLVILISGEFREVYLTQGELEINDRLQTLRALEDERRK	389	
DB	430	LDLMLRGHLISDIPILHDATRLVILISGEFREVYLTQGELEINDRLQTLRALEDERRK	489	
QY	390	TDITLTVSLPSPVANELRRKRPVPAKRDYNTILFSGIVGNACSKHASEGAMKIVNL	449	
DB	490	TYDLTSLIFPGVAQQLMGQGVQARRKEDYVLMFSDIVFTALCAQCT---PMQYISM	545	
QY	450	LDNLTRFRFDLIDSKRNPF--YKRYETVGDKMYVSGLPEPCIHMAISCHIALDMWEIA	507	
DB	546	LNELVYTRFD---HCCGFLDIYKVTETGDAVCVAAGLHRRSLCHAPITALMAKMWELS	600	
QY	508	GOVAV--DGESVQITITIHGEVYVTCVIGQPMRYCLFGNTVNLISRETTGEEKKINWSE	566	
DB	601	EEVLTPTDGRIDQIRISIHSGSVLACVAGVBMRYCLFGNNVTLASKRESSGHPRIINVP	660	
QY	567	YTYRCLMSPEPN 577		
DB	661	TYVQLKREBS 671		
RESULT 8				
CYG3_RAT	STANDARD;	PRT;	690 AA.	
AT	P19686;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Guanylate cyclase soluble, alpha-1 chain (EC 4.6.1.2) (GCS-alpha-1)			
DE	(Soluble guanylate cyclase large subunit).			
GN	GUCY1A1 OR GUCY1A1.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_Taxid=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RC	TISSUE=Lung;			
RX	MEDLINE=91009100; PubMed=1698769;			
RA	Nakane M., Arai K., Saheki S., Kuno T., Buechler W., Murad F.;			
RT	"Molecular cloning and expression of cDNAs coding for soluble			
RL	guanylate cyclase from rat lung."			
RL	J. Biol. Chem. 265:16841-16845(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			

RC STRAIN-Sprague-Dawley; TISSUE-Striatum;
RA MEDLINE-97151525; PubMed-8997507;
RX Smigrodzki R.M., Levitt P.;
RT "The alpha 1 subunit of soluble guanylyl cyclase is expressed
RT prenatally in the rat brain."
RL Brain Res. Dev. Brain Res. 97:226-234(1996).
CC -1- CATALYTIC ACTIVITY: GTP -> 3',5'-cyclic GMP + diphosphate.
CC -1- ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE OF
CC MAGNESIUM OR MANGANESE IONS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES: SOLUBLE
CC FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
CC -1- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
CC FAMILY.
CC -----
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CC -----
DR EMBL: M57405; AAA41206.1; -
DR EMBL: U60835; AAB17953.1; -
DR PIR: A38297; OYR1A1.
DR HSSP: P19687; 1AMN.
DR InterPro: IPR001054; G_Cyclase.
DR Pfam: PF00211; guanylate_cyc; 1.
DR SMART: SM00044; CYC; 1.
DR PROSITE: PS00452; GUANYLATE_CYCLASES_1; 1.
DR PROSITE: PS50125; GUANYLATE_CYCLASES_2; 1.
DR Lysase; CGMP synthetase; Multigene family.
KW DOMAIN 480 607 GUANYLATE CYCLASE.
FT SEQUENCE 690 AA; 77566 MW; E4819B2CAAF86401 CRC64;
SQ

Query Match 24.5%; Score 793; DB 1; Length 690;
Best Local Similarity 34.7%; Pred. No. 3.3e-47;
Matches 214; Conservative 100; Mismatches 215; Indels 88; Gaps 20;

OY 27 KRAQDESGPLVRIYDQSKTYDLYAASKVNLNAGELIQ-MGCKMFVYQSGEYDT 85
DB 102 KENRNSSEKEDERITAEBA-----TAAGVPV-----EVLDSJGEELFKCYEED-EH 149
OY 86 ILRLVGSNVRFLQNDAL-----HDHLATIPYGMKAPSFRTDAEKGILITHYSERE 140
DB 150 ILGVVGTLKDFLNSFSTLLKQSHQGEERGRLEDAIILCDKQ-DFLANYYTFPPRR 208
OY 141 GLQDIVIGITVAQOIHSTEDMKVYIQ-RNEEDHTQFL-----IEEKSEEDF 191
DB 209 TTAALLPGITKAAARILYSEHVESLMPCEFRSEC--TEFVNQPYLLGVHYKSTKPS-- 264
OY 192 YEDLDREENGQOESNISPYT-FCKAPPHIIFDRDLYVYQGNALYRVLQQL-PGNS 249
DB 265 -----LSFGKQSSIVLPTSLCKTFEPHMDRLALIQGNGIRLVNKRDFGKPN 318
OY 250 LLSVSLVRPHIDISFGHILSHINTVFLRSKEGLDVEKCEDELTEISCLRLKQ 309
DB 319 PEEFEILLPKINQTFSGIMTMNMQFVIRVRW-----DNLVKKSSRVMDLKQ 368
OY 310 MIYLPDASILFLCSPSVANLDDLRRGLYLSDIPLHADRDLVLLGEGFREERYKVLQEL 369
DB 369 MIYIYESSALFLFCPCVDRLEDFGRLGYLSDIPHNALRYVLLGEGQARADGDKRL 428
OY 370 ELVTRIQTLRLADEKKKTDLLYSVLPSPVANLRKRKRPAPARYNNTLFGSITG 429
DB 429 GELKATLEHAQALDEKKKTYDLCLSTIPSEVAQOLQGOIVQAKKEVYMLFSDIYG 488
OY 430 FNAFOSKSHASGAMKIVMLNDLYTRFDTLTDSRKNPVYKVEFYGDYMTYSGLPEDC 489
DB 489 FTAISQGS-----PIQVITMLNALVTRFQGGSELD--VYKVEITGDAYCAVAGIARRS 541

OY 490 IHHANISCHLADMEIAGOV-QVDESGVQITIGITGEVTVGICQMRPRCLFGNTVN 548
DB 542 DTHAVQIALMALKMEISNESPHEPIKMRIGLSSGVFAGVVKMRPRCLFGNTV 601
OY 549 LNSRTTEGKGINSEYTRCL-----NSPENSDFQ-----HL-----EH 586
DB 602 LANKFSCSVPRKINSPPTVRLKDCPGFVFTPRSRRELPPNPSDIPGICHLDAYOH 661
OY 587 RGPVSMKGRKEPMQVWF 603
DB 662 QGPN-----KPMF 670

RESULT 9
CYG3_HUMAN
ID CYG3_HUMAN STANDARD; PRT; 690 AA.
AC 002108; Q43843;
DT 01-JUL-1993 (Rel. 26, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Guanylate cyclase soluble, alpha-1 chain (EC 4.6.1.2) (GCS-alpha-1)
DE (Soluble guanylate cyclase large subunit) (GCS-alpha-3).
GN GUCY1A1 OR GUCY1A3 OR GUC1A3 OR GUCS3.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RX MEDLINE-92316204; PubMed-1352257;
RA Guilli G., Scholl U., Buile F., Guellaen G.;
RT Molecular cloning of the cDNAs coding for the two subunits of
RT soluble guanylyl cyclase from human brain.";
RL FEBS Lett. 304:83-88(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Kidney;
RA Ganssems Y., Brouckaert P., Fiers W.;
RT "Human soluble guanylate cyclase large subunit mRNA, alpha3-like.";
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RX MEDLINE-98416113; PubMed-9742212;
RA Zabel U., Weeger M., La M., Schmidt H.H.;
RT "Human soluble guanylate cyclase: functional expression and revised
RT isoenzyme family.";
RL Biochem. J. 335:51-57(1998).
CC -1- CATALYTIC ACTIVITY: GTP -> 3',5'-cyclic GMP + diphosphate.
CC -1- ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE OF
CC MAGNESIUM OR MANGANESE IONS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES: SOLUBLE
CC FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
CC -1- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
CC FAMILY.
CC -----
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CC -----
DR EMBL: X66534; CAA47145.1; -
DR EMBL: U58855; AAB94794.1; -
DR EMBL: Y15723; CAA75738.1; -
DR PIR: S23098; S23098.
DR HSSP: P19687; 1AMN.
DR Genew; HGNC:4685; GUCY1A3.

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Kidney;
 RX MEDLINE=89356605; PubMed=2569967;
 RA Lowe D.G., Chang M.S., Hellmias R., Chen E., Singh S., Garbers D.L.,
 RA Goeddel D.V.;
 RT "Human atrial natriuretic peptide receptor defines a new paradigm for
 RT second messenger signal transduction.";
 RL EMBO J. 8:1377-1384(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Blood;
 RX MEDLINE=98289600; PubMed=9618281;
 RA Takahashi Y., Nakayama T., Soma M., Izumi Y., Kamatsuse K.;
 RT "Organization of the human natriuretic peptide receptor A gene";
 RL Biochem. Biophys. Res. Commun. 246:736-739(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Maeda N., Knowles J.W.;
 RT "Identification of functional polymorphisms in noncoding regions of
 RT the human natriuretic peptide receptor A gene";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 634-1048 FROM N.A.
 RC TISSUE-Retina;
 RX MEDLINE=95042574; PubMed=7954658;
 RA Pardhasaradhi K., Kutty R.K., Gentileman S., Krishna G.;
 RT "Expression of mRNA for atrial natriuretic peptide receptor guanylate
 RT cyclase (ANPRA) in human retina";
 RL Cell. Mol. Neurobiol. 14:17(1994).
 CC -1- FUNCTION: RECEPTOR FOR ATRIAL NATRIURETIC PEPTIDE. HAS GUANYLATE
 CC CYCLASE ACTIVITY ON BINDING OF ANP.
 CC -1- CATALYTIC ACTIVITY: GTP -> 3',5'-cyclic GMP + diphosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- MISCELLANEOUS: THERE SEEM TO BE AT LEAST THREE ANP RECEPTORS: TWO
 CC WITH GUANYLATE CYCLASE ACTIVITY (ANP-A AND ANP-B) AND ONE (ANP-C)
 CC WHICH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF ANP FROM THE
 CC CIRCULATION WITHOUT A ROLE IN SIGNAL TRANSDUCTION.
 CC -1- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
 CC FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 PROTEIN KINASE-LIKE DOMAIN.
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DR EMBL; AB010490; BAA31199.1; JOINED.
 DR EMBL; AF190631; AA01340.1; -.
 DR EMBL; S72628; AAD14112.1; -.
 DR PIR; S04459; OYHUR.
 DR HSSP; 002846; 1AML.
 DR GeneW; HGNC:7943; NPRL.
 DR MIM; 108960; -.
 DR InterPro; IPR001828; ANP_receptor.
 DR InterPro; IPR000719; Euk_kinase.
 DR InterPro; IPR001054; G_cyclase.
 DR InterPro; IPR001170; Ntpep_receptor.
 DR Pfam; PF00069; kinase; 1.
 DR Pfam; PF00211; guanylate_cyc; 1.
 DR Pfam; PF01094; ANP_receptor; 1.
 DR PRINTS; PR00255; NATPEPTIDER.
 DR ProDom; PD000001; Euk_kinase; 1.
 DR SMART; SM00044; CycC; 1.
 DR PROSITE; PS00458; ANP_RECEPTORS; 1.
 DR PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.
 DR PROSITE; PS00125; GUANYLATE_CYCLASES_2; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW Receptor; Transmembrane; Glycoprotein; Phosphorylation; Lyase;
 KW GMP synthesis; Signal.
 FT SIGNAL 1..32
 FT CHAIN 33..1061
 FT DOMAIN 33..473
 FT TRANSMEM 474..494
 FT DOMAIN 495..1061
 FT DOMAIN 528..805
 FT DOMAIN 876..1006
 FT DISULFID 92..118
 FT DISULFID 196..245
 FT DISULFID 455..455
 FT DISULFID 464..464
 FT CARBOHYD 34..34
 FT CARBOHYD 45..45
 FT CARBOHYD 212..212
 FT CARBOHYD 338..338
 FT CARBOHYD 379..379
 FT CARBOHYD 386..386
 FT CARBOHYD 427..427
 SEQUENCE 1061 AA; 118918 MW; E65BD0FCA32F70D CR664;
 Query Match 14.98; Score 481.5; DB 1; Length 1061;
 Best Local Similarity 27.7%; Pred. No. 1.8e-25;
 Matches 197; Conservative 88; Mismatches 227; Indels 199; Gaps 31;
 OY 33 EESGIVIRITIDDKETDVLVAASKVIN-----LNAGEI 66
 DB 416 ENGAFRYVLTNTNGT-SQELVAVSGRKLWPLGTPPPDIPKCGFNEDPACNODHLSTLEY 474
 OY 67 LQMPGKM-----FFVF-----COESGYDILRVLSNVEFLQNLDAHDAHTIYP 113
 DB 475 LALVGSILGLILVSPFYRKQMLEKELASLRVREHDEVP-----SSLERL----- 524
 OY 114 GMRAPSRCTDAENGK--GLILHYSEREGQDIYIGIKTVAAQIHGTETDMKVYIQRN 171
 DB 525 --RSAGSNLTLSGSGSNVSL-----TTEGGQFV--FAKAYYK--GNLVAVRVYKR 573
 OY 172 EECGTOFLIEKSKEDFEYEDLRPEENGTOSRSIPY--FEKAPFHIIIPRDLYVT 230
 DB 574 IEL--TRVYLELKHMDVONEHLTRVYGACTDPNPICTLEYCPRGSLDILENESTTL 631
 OY 231 -----OCGNAIVFVLPOLOPGN-CSLVSFSLVRPHIDISFGILSHINTV-----FVLR 279
 DB 632 DMMFRYSLTNDIVAGMFLHNGAICS-----HONLSSNVCVVDGRVYVK 675
 OY 280 SKE-GLADVEKLECEDELGTETISCLRLKGMIT--LPEADSLFLCSPSV--MNTDDL 333
 DB 676 ITDYGLESFRDLDE-----QGHTVYAKKIMTAPPELLRMAAPVRGSSQAGDV 722
 OY 334 TRRGVLSDFPL-----HDATRD-----VLGRQ--FREYKTLQLEEL----- 372

Db 723 YSFGIILQEIARSGFVHVEGLDSPKEIIEVTVNGEPPFRPSLALQSHLEELIMOR 782
 Qy 373 -----TRDQLTLR-----ALDEK 387
 Db 783 CWAEDPQERPPQQLRLTKRFRRENSNILDNLRLMDOYANNLEELVEERTQAVLEEK 842
 Qy 388 KTDPLLSVLPSPVANEIRKRPAPAKRYDNTILFSGIVGFNACSHASGEGAMKIV 447
 Db 843 RAKEALLVQILPHSAEQLRKGEVQAEFDSVTTFPSIDVFTALSAEST-----PMQV 898
 Qy 448 NLINDLYRFDLTDSRKNPFYKVEYGDKNYMTVSGLEPEPCIH-----HARSICHTALIM 503
 Db 899 TLINDLYTCFDAVID---NEDYKVEITGDALMVVSGLP---VRNGRLHACEYARALAL 952
 Qy 504 MEIAQOVQV---DGSVQITIGIHGEVVTGVIGOMPRYCEFGNTVNLTSRTETTGEGK 560
 Db 953 IDAVSFRIRHRPQDLRLRIGIHGPGVAGVGLKMPRYCEFGDVTVMASRESNGEAL 1012
 Qy 561 KINSEYTYRCIMSPENSDPQHLERHGVSKGKKEPQVWFLSKKNTGT 611
 Db 1013 KIHLSSETKAVL-----EEFGFELRLGDEVMKKGKRVTYMLGERSST 1059

RESULT 13

ANPA_RAT STANDARD; PRT; 1057 AA.

AC P18910;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Atrial natriuretic peptide receptor A precursor (ANP-A) (ANPRA) (GC-A) (Guanlylate cyclase) (EC 4.6.1.2) (NPR-A) (Atrial natriuretic peptide A-type receptor).
 GN NPR1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA MEDLINE=89143770; PubMed=2563900;
 RA Chinkers M., Garbers D.L., Chang M.S., Lowe D.G., Chin H., Goeddel D.V., Schulz S.;
 RT "A membrane form of guanylate cyclase is an atrial natriuretic peptide receptor.";
 RN Nature 338:78-83(1989).
 RP SEQUENCE FROM N.A.
 RA MEDLINE=91056089; PubMed=1978722;
 RA Yamaguchi M., Rutledge L.J., Garbers D.L.;
 RT "The primary structure of the rat guanylyl cyclase A/atrial natriuretic peptide receptor gene.";
 RN J. Biol. Chem. 265:20414-20420(1990).
 RP [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91352095; PubMed=1679239;
 RA Duda T., Goraczniak R.M., Sharma R.K.;
 RT "Site-directed mutational analysis of a membrane guanylate cyclase cDNA reveals the atrial natriuretic factor signaling site.";
 RN Proc. Natl. Acad. Sci. U.S.A. 88:7882-7886(1991).
 CC -1- FUNCTION: RECEPTOR FOR ATRIAL NATRIURETIC PEPTIDE. HAS GUANYLATE CYCLASE ACTIVITY ON BINDING OF ANP.
 CC -1- CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + diphosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- MISCELLANEOUS: THERE SEEM TO BE AT LEAST THREE ANP RECEPTORS: TWO WITH GUANYLATE CYCLASE ACTIVITY (ANP-A AND ANP-B) AND ONE (ANP-C) WHICH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF ANP FROM THE CIRCULATION WITHOUT A ROLE IN SIGNAL TRANSDUCTION.
 CC -1- SIMILARITY: SOME SIMILARITY WITH CONSERVED REGION OF CATALYTIC DOMAIN OF PROTEIN KINASES.
 CC -1- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE FAMILY.

CC -1- SIMILARITY: CONTAINS 1 PROTEIN KINASE-LIKE DOMAIN.
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 DR EMBL: X14773; CAA32881.1; -
 DR EMBL: J05677; AAA11200.1; -
 DR EMBL: M74535; AAA11202.1; -
 DR PIR: S03348; OYTR.
 DR HSSP: Q02846; IAWL.
 DR InterPro: IPR001828; ANF_receptor.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR001054; G_cyclase.
 DR InterPro: IPR001170; Ntpep_receptor.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF01094; guanylate_cyc; 1.
 DR PRINTS: PR00255; NATEPTIDER.
 DR PRODOM: PD000001; Euk_pkinase; 1.
 DR SMART: SM00044; CYCC; 1.
 DR PROSITE: PS00458; ANF_RECEPTORS; 1.
 DR PROSITE: PS00452; GUANYLATE_CYCLASES_1; 1.
 DR PROSITE: PS50125; GUANYLATE_CYCLASES_2; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW Receptor; Transmembrane; Glycoprotein; Phosphorylation; Lyase; GMP synthetis; Signal.
 FT SIGNAL 1 28
 FT CHAIN 29 1057
 FT DOMAIN 29 469
 FT TRANSMEM 470 490
 FT DOMAIN 491 1057
 FT DOMAIN 524 801
 FT DOMAIN 872 1002
 FT DISULFID 88 114
 FT DISULFID 192 241
 FT DISULFID 451 451
 FT DISULFID 460 460
 FT CARBOHYD 41 41
 FT CARBOHYD 208 208
 FT CARBOHYD 334 334
 FT CARBOHYD 375 375
 FT CARBOHYD 382 382
 FT CARBOHYD 423 423
 FT CONFLICT 366 366
 FT CONFLICT 392 392
 SQ SEQUENCE 1057 AA; 118951 MW; 9EA9AE685AC05816 CRC64;
 Query Match 14.5%; Score 468; DB 1; Length 1057;
 Best Local Similarity 43.4%; Pred. No. 1.6e-24;
 Matches 112; Conservative 38; Mismatches 82; Indels 26; Gaps 9;
 Qy 361 EEEKLTQDEILTRDQLTLRALEDKKKTDLLSVLPSPVANEIRKRPAPAKRYDNY 420
 Db 817 EGYANMLE-ELVEREQAVL-----EERKRAELLYQILPHSAEQLRKGEVQAEFDSV 871
 Qy 421 TLFSGIVGFNACSHASGEGAMKIVNLINDLYRFDLTDSRKNPFYKVEYGDKNY 480
 Db 872 TLFSGIVGFNALSAST-----PMQVTLINDLYRFDLTDSRKNPFYKVEYGDKNY 924
 Qy 481 TVSGLEPEPCIH-----HARSICHTALIMMEIAQOVQV---DGSVQITIGIHGEVVTGV 533
 Db 925 VVSGLP---VRNGRLHACEYARALALDLNLSRFRIRHRPQDLRLRIGIHGPGVAGV 981
 Qy 534 GQMPRYCEFGNTVNLTSRTETTGEGKIVSEYTYRCIMSPENSDPQHLERHGVSK 593
 Db 982 GLKMPRYCEFGDVTVMASRESNGEALKIHLSSETKAVL---BEFD-GFLELRGVEMK 1037
 Qy 594 GKKEPQVWFLSKKNTGT 611

Db 1038 GRKGVRTYWLGERGCS 1055

RESULT 14

ANPA_MOUSE STANDARD; PRT: 1057 AA.

ID ANPA_MOUSE

AC P18293;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Atrial natriuretic peptide receptor A precursor (ANP-A) (ANPRA) (GC-A)

DE (guanylate cyclase) (EC 4.6.1.2) (NPR-A) (Atrial natriuretic peptide A-type receptor).

GN NPRI OR NPRA.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RC SEQUENCE FROM N.A.

RP STRAIN=C57BL/6J;

RX MEDLINE=90324219; PubMed=1973687;

RA Pandey K.N., Singh S.;

RT "Molecular cloning and expression of murine guanylate cyclase/atrial natriuretic factor receptor cDNA.";

RL J. Biol. Chem. 265:12342-12348(1990).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=95139994; PubMed=7838126;

RA Schoenfeld J.R., Sehl P., Quan C., Burnier J.P., Lowe D.G.;

RT "Agonist selectivity for three species of natriuretic peptide receptor-A.";

RL Mol. Pharmacol. 47:1172-180(1995).

CC -1 FUNCTION: RECEPTOR FOR ATRIAL NATRIURETIC PEPTIDE. HAS GUANYLATE CYCLASE ACTIVITY ON BINDING OF ANP.

CC -1 CATALYTIC ACTIVITY: GTP -> 3',5'-cyclic GMP + diphosphate.

CC -1 SUBCELLULAR LOCATION: Type I membrane protein.

CC -1 MISCELLANEOUS: THERE SEEM TO BE AT LEAST THREE ANP RECEPTORS: TWO WITH GUANYLATE CYCLASE ACTIVITY (ANP-A AND ANP-B) AND ONE (ANP-C) WHICH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF ANP FROM THE CIRCULATION WITHOUT A ROLE IN SIGNAL TRANSDUCTION.

CC -1 SIMILARITY: BELONGS TO ADENYLATE CYCLASE CLASS-4/GUANYLATE CYCLASE FAMILY

CC -1 SIMILARITY: CONTAINS 1 PROTEIN KINASE-LIKE DOMAIN.

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CC EMBL: J05504; AAA37670.1; -

CC EMBL: L31937; AAA66945.1; -

CC PIR: A36568; OTMSAR.

CC PIR: A33088; A33088.

CC HSSP: Q02846; IAWL.

CC MGD: MGI:97371; NPRL.

CC InterPro: IPR001828; ANF_receptor.

CC InterPro: IPR000719; Euk_kinase.

CC InterPro: IPR001054; G_cyclase.

CC InterPro: IPR001170; Ntpep_receptorN.

CC Pfam: PF00069; pkinase; 1.

CC Pfam: PF00211; guanylate_cyc; 1.

CC Pfam: PF01094; ANF_receptor; 1.

CC PRINTS: PR00255; NATPEPTIDER.

CC PRODOM: PD000001; Euk_pkinase; 1.

CC SMART: SM00044; CYCC; 1.

CC PROSITE: PS00458; ANF_RECEPTORS; 1.

CC PROSITE: PS00452; GUANYLATE_CYCLASES_1; 1.

CC PROSITE: PS00125; GUANYLATE_CYCLASES_2; 1.

DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.

KW Receptor; Transmembrane; Glycoprotein; Phosphorylation; Tyase;

KW CGMP synthesis; Signal.

FT SIGNAL 1 28

FT CHAIN 29 1057

FT DOMAIN 29 469

FT TRANSMEM 470 490

FT DOMAIN 491 1057

FT DOMAIN 524 801

FT DOMAIN 872 1002

FT DISULFID 88 114

FT DISULFID 192 241

FT DISULFID 451 451

FT DISULFID 460 460

FT CARBOHYD 41 41

FT CARBOHYD 208 208

FT CARBOHYD 334 334

FT CARBOHYD 375 375

FT CARBOHYD 382 382

FT CARBOHYD 423 423

FT CONFLICT 3 3

FT CONFLICT 39 39

FT CONFLICT 122 122

FT CONFLICT 130 130

FT CONFLICT 285 285

FT CONFLICT 301 301

FT CONFLICT 404 405

FT CONFLICT 590 590

FT CONFLICT 590 590

FT CONFLICT 652 652

FT CONFLICT 833 833

FT CONFLICT 958 958

FT CONFLICT 1044 1044

FT CONFLICT 1050 1050

FT CONFLICT 1055 1057

SO SEQUENCE 1057 AA; 119109 MW; 53A544FB2C8FE253 CMC64;

Query Match 14.48; Score 466; DB 1; Length 1057;

Best Local Similarity 28.48; Pred. No. 2; 1e-24;

Matches 190; Conservative 86; Mismatches 210; Indels 182; Gaps 32;

25 IRKEADLDEE-GQFLVRIITDSDKTYDL---VAASKVNL-----NAGEIILQMPKMF 75

489 IYKMKLEKELVSELMKRVKREDLPSSLEHNLASASRLTSLRGSNGSLTTEQ-FO 547

76 VFCQESGYD---TILRVIGSNV---REFLQNT---DALHDLATIPQMRAPSPRCND 124

548 VFAKTAIVYKGNLVAVRKVRKRIELTRKVLFEKHKRDQVNEHL-TRFVG-----ACID 600

125 AERGRLLIHYEREGLDIVG-----IYTV-----AQIING--- 159

601 PP-NICILTEYCPKSLDILLENESITLDMWERYSLTNDIVGMLFLHNGAIGSHGNLK 658

160 -----TEIDMKVIOQRNECDHPFLIEEKSKREDYEDIDRPEE---NG 202

659 SSNCVVDGKRVLKITTYGLESPDPPEEGHTLF-----AKLMTAPELIRASAPRAG 712

203 TQESRISPYTFCKAFPHIIFRDVLVYTOG-----NAIYRLPOLQPGNCST 250

713 SQAGDV-----YSGFIIIGLQ--IALRSGVYVYEGLDLSPKEILERTVTRGQPP----- 758

251 LSVFSLVRPHIDISFGILSHITVTVVLSKESGLLVYKLECDDELGTETISCLRLKGM 310

759 -----FRPSMDQ-----SHLEELQOL-----MORWADBPDRPPQOIRLALKR 799

311 IYLPKADSLIFLCSFSPVNMIDDLTRGVLISDIPLDADRDVLGLGQFPEEYKLNQDE 370

800 EKNENSNT-----LDNLISK-----MEQYANLLE-E 825

371 IITDRLQTLRALDEKKRTDILLVSLPPSVANELRHRPYPARKRYDNTVILFSGIVGF 430

826 IVEREQAVL-----EKKRAEALLYQILPHSVAEQLKRGETVOAEAFDSVTIYFSDIVGF 881

431 MAFCSKHAEGEGAMKIVNLNDLITRFDTLTDKRNKPFYKYETVGDKTMYVSGLEPCTI 490

Db 1007 DAL---DELGCFOLELRGDVEMKKGCMRTYWLIGER 1040

Search completed: June 27, 2003, 13:03:29
Job time : 12.9305 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2003, 13:00:58 ; Search time 31.2101 Seconds

(Without alignments)
4086.601 Million cell updates/sec

Title: US-09-762-767a-4

Perfect score: 3231
Sequence: 1 MYGFVNHALLELVIRNGPE.....QWFLSRKNTGTETKQDD 619

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: SP:archaea:*
2: SP:bacteria:*
3: SP:fungi:*
4: SP:human:*
5: SP:invertebrate:*
6: SP:mammal:*
7: SP:mnc:*
8: SP:organelle:*
9: SP:phage:*
10: SP:plant:*
11: SP:rodent:*
12: SP:virus:*
13: SP:vertebrate:*
14: SP:unclassified:*
15: SP:rvirus:*
16: SP:bacteriaph:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3198	99.0	620	11	O54865 mus musculu
2	2887	89.4	614	13	P79998 oryzias lat
3	2859	88.5	617	13	O90VY5 fugu rubrip
4	1903.5	58.9	600	5	O77106 manduca sex
5	1883	58.3	758	5	O24086 drosophila
6	1883	57.9	787	5	O9VA09 drosophila
7	1870.5	57.9	604	5	O95NK5 hemicephal
8	1761	54.5	649	5	O17010 anopheles g
9	1105	34.2	742	11	O91XJ7 rattus norv
10	983	30.4	636	11	O92001 rattus norv
11	960.5	29.7	685	5	O9XTE0 caenorhabd
12	955	29.6	686	5	P92006 caenorhabd
13	955	29.6	940	5	O76340 manduca sex
14	938	29.0	751	5	O02298 caenorhabd
15	929.5	28.8	750	5	O9YFCS drosophila
16	914	28.3	699	5	O17707 caenorhabd

17	912.5	28.2	684	5	O9B180	O9B180 caenorhabd
18	788	24.4	564	4	O9NNW8	O9NNW8 homo sapien
19	788	24.4	675	13	O90VW5	O90VW5 fugu rubrip
20	786.5	24.3	690	4	O8TAH3	O8TAH3 homo sapien
21	783	24.2	678	13	O9PM12	O9PM12 oryzias lat
22	778	24.1	678	13	P79997	P79997 oryzias lat
23	778	24.1	691	11	O9DBQ3	O9DBQ3 mus musculu
24	778	24.1	691	11	O9ERL9	O9ERL9 mus musculu
25	757	23.4	699	5	O77105	O77105 manduca sex
26	729.5	22.6	752	5	O22301	O22301 caenorhabd
27	726	22.5	676	5	O24085	O24085 drosophila
28	720	22.3	676	5	O95S04	O95S04 drosophila
29	704.5	21.8	669	5	O9VEU5	O9VEU5 drosophila
30	701.5	21.7	583	5	O44468	O44468 caenorhabd
31	685	21.2	649	5	O9VEU6	O9VEU6 drosophila
32	646.5	20.0	947	5	P90895	P90895 caenorhabd
33	565	17.5	108	6	O8SPV3	O8SPV3 ovis aries
34	493	15.3	220	11	O8R5L4	O8R5L4 rattus norv
35	490.5	15.2	1070	13	O93490	O93490 anguilla ja
36	478.5	14.8	1126	5	O9BPR0	O9BPR0 bombyx mori
37	472	14.6	1055	13	O98U11	O98U11 oryzias lat
38	471	14.6	1055	13	O9YGM3	O9YGM3 oryzias lat
39	470	14.5	1057	5	O18331	O18331 caenorhabd
40	469.5	14.5	1052	13	O90YB7	O90YB7 rana catesb
41	467.5	14.5	1276	5	O878L6	O878L6 caenorhabd
42	466	14.4	1057	11	O91X04	O91X04 mus musculu
43	464	14.4	1047	13	O9PMH0	O9PMH0 xenopus lae
44	458	14.2	1076	5	O9VFI9	O9VFI9 drosophila
45	456.5	14.1	632	5	O94429	O94429 ctoma intes

ALIGNMENTS

RESULT 1

ID O54865 PRELIMINARY; PRT; 620 AA.

AC O54865;

DT 01-JUN-1998 (TREMBLrel. 06, Created)

DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Soluble guanylate cyclase beta-1 subunit.

GN GUCY1B3 OR GC-S-BETA-1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=LUNG;

RA Gansemans Y., Brouckaert P., Fiers W.;

RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/10;

RA Sharina I.G., Krumenacker J.S., Martin E., Murad F.;

RT "Genomic organization of alpha 1 and beta 1 subunits of the mammalian

Proc. Natl. Acad. Sci. U.S.A. 97:10878-10883(2000).

DR EMBL; AF020339; AAB94876.1; -

DR EMBL; AF297083; AAG17447.1; -

DR HSSP; P16068; IAWN.

DR MGD; MGI:1860604; Gucylb3.

DR InterPro: IPR001054; G_cyclase.

DR Pfam: PF00211; guanylate_cyc; 1.

DR SMART; SM00044; CYCC; 1.

DR PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.

DR PROSITE; PS0125; GUANYLATE_CYCLASES_2; 1.

KW Lyase.

SO SEQUENCE 620 AA; 70597 MW; EED9BAF53F4EF9 CRC64;

Query Match

99.0%; Score 3198; DB 11; Length 620;

Best Local Similarity 98.9%; Pred. No. 3,1e-233;
Matches 612; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MYGFVNHALBLVIRNYGPEWEDIKKEAQLDEGQFLVRIIYDSTKYDVAASRYLN 60
RT 1 MYGFVNHALBLVIRNYGPEWEDIKKEAQLDEGQFLVRIIYDSTKYDVAASRYLN 60
RT 1 MYGFVNHALBLVIRNYGPEWEDIKKEAQLDEGQFLVRIIYDSTKYDVAASRYLN 60
DB 1 MYGFVNHALBLVIRNYGPEWEDIKKEAQLDEGQFLVRIIYDSTKYDVAASRYLN 60
QY 61 LNAGEIIOFMGKMFVFCQSGYDTILRVGNSVREFLQNDLHDLHATITPGMAPSF 120
DB 61 LNAGEIIOFMGKMFVFCQSGYDTILRVGNSVREFLQNDLHDLHATITPGMAPSF 120
QY 121 RCTDAEKGKLLIHYSEREGLODIYGIITKTAQOIHGEIDMKVIOQNEEDHPOFL 180
DB 121 RCTDAEKGKLLIHYSEREGLODIYGIITKTAQOIHGEIDMKVIOQNEEDHPOFL 180
QY 181 IEERSEKEDFYEDLDQFEENGTOESRISPYTECKAPFPHIIPDRDLVVOGNAIYRVL 240
DB 181 IEERSEKEDFYEDLDQFEENGTOESRISPYTECKAPFPHIIPDRDLVVOGNAIYRVL 240
QY 241 POLQPGNCSLVPSVLRPHIDISFNGILSHINTVFLRSKREGLLDYKLECEDELGTGE 300
DB 241 POLQPGNCSLVPSVLRPHIDISFNGILSHINTVFLRSKREGLLDYKLECEDELGTGE 300
QY 301 ISCLRLKGOMIYLPBADSILFLCSPSVANLDDLTRRGLYSDIPLHDATDVLVLEQFR 360
DB 301 ISCLRLKGOMIYLPBADSILFLCSPSVANLDDLTRRGLYSDIPLHDATDVLVLEQFR 360
QY 361 EBYKLTQELILDLRLQTLRALEDEKKTDLLYSVLPSPVANLHKKRPVPAKRDYV 420
DB 361 EBYKLTQELILDLRLQTLRALEDEKKTDLLYSVLPSPVANLHKKRPVPAKRDYV 420
QY 421 TIFSGIVGNFNAFCSKRASEGAMKTYNLNDLITRPTDITDSKNFVYKVEYGDQRYM 480
DB 421 TIFSGIVGNFNAFCSKRASEGAMKTYNLNDLITRPTDITDSKNFVYKVEYGDQRYM 480
QY 481 TVSGLPSPCHHARSICHLALDMMETAGOVQVDESQITIGITGEGVYGVIGORRPXY 540
DB 481 TVSGLPSPCHHARSICHLALDMMETAGOVQVDESQITIGITGEGVYGVIGORRPXY 540
QY 541 CLFGNTVNLTSRPTTEGKINVSERYTRCLMSPENDPOFILHHRGPVSMGKKEPMQ 600
DB 541 CLFGNTVNLTSRPTTEGKINVSERYTRCLMSPENDPOFILHHRGPVSMGKKEPMQ 600
QY 601 VWFLSRKNTGTEETKODD 619
DB 601 VWFLSRKNTGTEETNEDE 619

RESULT 2
P79998 PRELIMINARY; PRT; 614 AA.

AC P79998;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Soluble guanylyl cyclase beta subunit (BC 4.6.1.2).
OS Oryzias latipes (Medaka fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Atherinomorpha;
OC Belontiiformes; Adrianchthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98237571; PubMed=9578459;
RA Mikami T., Kusakabe T., Suzuki N.;
RT Molecular cloning of cDNAs and expression of mRNAs encoding alpha and
RT beta subunits of soluble guanylyl cyclase from medaka fish *Oryzias*
RT latipes.
RL Eur. J. Biochem. 253:42-48(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99303623; PubMed=10373466;

RA Mikami T., Kusakabe T., Suzuki N.;
RT "Random organization of medaka fish soluble guanylyl cyclase alpha
RT and beta subunit genes. Implications for coordinated transcription of
RT two subunit genes."
J. Biol. Chem. 274:18567-18573(1999).
DR EMBL: AB000850; BAA19199.1;
DR EMBL: AB022281; BAA76691.1;
DR HSSP: P16068; 1AMN.
DR InterPro: IPR001054; G_cyclase.
DR Pfam: PF00211; guanylate_cyc.1.
DR SMART: SM00044; CYC.1.
DR PROSITE: PS00452; GUANYLATE_CYCLASES_1; 1.
DR PROSITE: PS0125; GUANYLATE_CYCLASES_2; 1.
SQ Lysase.
SEQUENCE 614 AA; 69917 MW; 64EDF9452D4714C1 CRC64;

Query Match 89.4%; Score 2887; DB 13; Length 614;
Best Local Similarity 89.2%; Pred. No. 9.8e-210; Indels 0; Gaps 0;
Matches 547; Conservative 37; Mismatches 29;

QY 1 MYGFVNHALBLVIRNYGPEWEDIKKEAQLDEGQFLVRIIYDSTKYDVAASRYLN 60
DB 1 MYGFVNHALBLVIRNYGPEWEDIKKEAQLDEGQFLVRIIYDSTKYDVAASRYLN 60
QY 61 LNAGEIIOFMGKMFVFCQSGYDTILRVGNSVREFLQNDLHDLHATITPGMAPSF 120
DB 61 LNAGEIIOFMGKMFVFCQSGYDTILRVGNSVREFLQNDLHDLHATITPGMAPSF 120
QY 121 RCTDAEKGKLLIHYSEREGLODIYGIITKTAQOIHGEIDMKVIOQNEEDHPOFL 180
DB 121 RCTDAEKGKLLIHYSEREGLODIYGIITKTAQOIHGEIDMKVIOQNEEDHPOFL 180
QY 181 IEERSEKEDFYEDLDQFEENGTOESRISPYTECKAPFPHIIPDRDLVVOGNAIYRVL 240
DB 181 IEERSEKEDFYEDLDQFEENGTOESRISPYTECKAPFPHIIPDRDLVVOGNAIYRVL 240
QY 241 POLQPGNCSLVPSVLRPHIDISFNGILSHINTVFLRSKREGLLDYKLECEDELGTGE 300
DB 241 POLQPGNCSLVPSVLRPHIDISFNGILSHINTVFLRSKREGLLDYKLECEDELGTGE 300
QY 301 ISCLRLKGOMIYLPBADSILFLCSPSVANLDDLTRRGLYSDIPLHDATDVLVLEQFR 360
DB 301 ISCLRLKGOMIYLPBADSILFLCSPSVANLDDLTRRGLYSDIPLHDATDVLVLEQFR 360
QY 361 EBYKLTQELILDLRLQTLRALEDEKKTDLLYSVLPSPVANLHKKRPVPAKRDYV 420
DB 361 EBYKLTQELILDLRLQTLRALEDEKKTDLLYSVLPSPVANLHKKRPVPAKRDYV 420
QY 421 TIFSGIVGNFNAFCSKRASEGAMKTYNLNDLITRPTDITDSKNFVYKVEYGDQRYM 480
DB 421 TIFSGIVGNFNAFCSKRASEGAMKTYNLNDLITRPTDITDSKNFVYKVEYGDQRYM 480
QY 481 TVSGLPSPCHHARSICHLALDMMETAGOVQVDESQITIGITGEGVYGVIGORRPXY 540
DB 481 TVSGLPSPCHHARSICHLALDMMETAGOVQVDESQITIGITGEGVYGVIGORRPXY 540
QY 541 CLFGNTVNLTSRPTTEGKINVSERYTRCLMSPENDPOFILHHRGPVSMGKKEPMQ 600
DB 541 CLFGNTVNLTSRPTTEGKINVSERYTRCLMSPENDPOFILHHRGPVSMGKKEPMQ 600
QY 601 VWFLSRKNTGTEE 613
DB 601 VWFLSRKSSDADK 613

RESULT 3
Q90YV5 PRELIMINARY; PRT; 617 AA.

AC Q90YV5;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Soluble guanylyl cyclase beta subunit.

GN FRGS-BETA1.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Takifugu.
 NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Morinaga C., Yamamoto T., Moriya Y., Suzuki N.;
 RT Identification of tandem organization of soluble guanylyl cyclase
 RT alpha1 and beta1 subunit genes in the Japanese pufferfish (Fugu
 RT rubripes) genome.
 RL Submitted (Mar-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB062172; BAB60908.1; -
 DR EMBL; AB062170; BAB60906.1; -
 DR InterPro: IPR001054; G_cyclase.
 DR InterPro: IPR000834; Zn_carboxypept.
 DR Pfam: PF00211; guanylate_cyc; 1.
 DR PROSITE: PS00132; CARBOXYPEPT_2N_1; UNKNOWN_1.
 DR PROSITE: PS00452; GUANYLATE_CYCLASES_1; UNKNOWN_1.
 DR PROSITE: PS00125; GUANYLATE_CYCLASES_2; 1.
 SQ SEQUENCE 617 AA; 70236 MW; 7B531B5896A06191 CRC64;

Query Match 88.5%; Score 2859; DB 13; Length 617;
 Best Local Similarity 88.7%; Pred. No. 1.3e-207;
 Matches 540; Conservative 41; Mismatches 28; Indels 0; Gaps 0;

1 MGFVNAHELELVIRNYGPEWEDIKKKAQDEEGFLVRIYDSKTYDLVAASKVYN 60
 1 MGFVNAHELELVIRNYGPEWEDIKKKAQDEEGFLVRIYDSKTYDLVAASKVYN 60
 61 IDAGDILQFGKMFEEFCQESGYDTLIRVLSNVREFLQNDLHDLHGLTIYGMKAPSP 120
 61 IDAGDILQFGKMFEEFCQESGYDTLIRVLSNVREFLQNDLHDLHGLTIYGMKAPSP 120
 121 RCTDAEKKGKGLLHYHSEREGLODIYIGIKTYAAQIHGTEIDMKYIOORNECDHTOFL 180
 121 RCTDAEKKGKGLLHYHSEREGLODIYIGIKTYAAQIHGTEIDMKYIOORNECDHTOFL 180
 121 RCTDAEKKGKGLLHYHSEREGLODIYIGIKTYAAQIHGTEIDMKYIOORNECDHTOFL 180
 181 IEKSKEDFEYDLDREFENGQESRISPYTFCKAFPHIIFDRDLVYTOGNAIYRYL 240
 181 IEKSKEDFEYDLDREFENGQESRISPYTFCKAFPHIIFDRDLVYTOGNAIYRYL 240
 181 IEKSKEDFEYDLDREFENGQESRISPYTFCKAFPHIIFDRDLVYTOGNAIYRYL 240
 181 IEKSKEDFEYDLDREFENGQESRISPYTFCKAFPHIIFDRDLVYTOGNAIYRYL 240
 241 POLQPCNSLVSFSLVRPHIDISFGILSHINTVFLSKEGLDVKECEDELGTGE 300
 241 POLQPCNSLVSFSLVRPHIDISFGILSHINTVFLSKEGLDVKECEDELGTGE 300
 241 POLQPCNSLVSFSLVRPHIDISFGILSHINTVFLSKEGLDVKECEDELGTGE 300
 241 POLQPCNSLVSFSLVRPHIDISFGILSHINTVFLSKEGLDVKECEDELGTGE 300
 301 ISCLRKGOMIYLPKADSLIFLCSPSVMNLDLTRGLYLSIDPLDARFDVLLGEQFR 360
 301 ISCLRKGOMIYLPKADSLIFLCSPSVMNLDLTRGLYLSIDPLDARFDVLLGEQFR 360
 301 ISCLRKGOMIYLPKADSLIFLCSPSVMNLDLTRGLYLSIDPLDARFDVLLGEQFR 360
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 361 EEYKLTQELIETDLRQLTLRALDEKKKTDTLLYSVLPPSVANELRHRPVPARYKDY 420
 361 EEYKLTQELIETDLRQLTLRALDEKKKTDTLLYSVLPPSVANELRHRPVPARYKDY 420
 361 EEYKLTQELIETDLRQLTLRALDEKKKTDTLLYSVLPPSVANELRHRPVPARYKDY 420
 361 EEYKLTQELIETDLRQLTLRALDEKKKTDTLLYSVLPPSVANELRHRPVPARYKDY 420
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 421 TILFSGIVGFNAFCSKHASGEGAMKIVNLNDLYTRFDLTDSKKNPFYKYVGVGDKYM 480
 421 TILFSGIVGFNAFCSKHASGEGAMKIVNLNDLYTRFDLTDSKKNPFYKYVGVGDKYM 480
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 541 CLFGNTVNLTSRTEETGEGKINVSRYTYRCLMSPNSDPOFLHREGVSMKGKREPMO 600
 541 CLFGNTVNLTSRTEETGEGKINVSRYTYRCLMSPNSDPOFLHREGVSMKGKREPMO 600
 541 CLFGNTVNLTSRTEETGEGKINVSRYTYRCLMSPNSDPOFLHREGVSMKGKREPMO 600
 601 VWFLSRKNP 609
 601 VWFLSRKNP 609
 601 VWFLSRKNP 609
 601 VWFLSRKNP 609

RESULT 4
 ID 077106 PRELIMINARY; PRT; 600 AA.
 AC 077106;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Soluble guanylyl cyclase beta-1 subunit.
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC SpHINGIDAE; SpHINGIDAE; SpHINGIDAE; Manduca.
 NCBI_TaxID=7130;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-98409773; PubMed-9736646;
 RA Nighorn A., Gibson N.J., Rivers D.M., Hildebrand J.G., Motton D.B.;
 RT "The nitric oxide-cGMP pathway may mediate communication between
 RT sensory afferents and projection neurons in the antennal lobe of
 RT manduca sexta."
 RL J. Neurosci. 18:7244-7255(1998).
 DR EMBL; AF062751; AAC61264.1; -
 DR HSSP; P16068; IAWN.
 DR InterPro: IPR001054; G_cyclase.
 DR Pfam: PF00211; guanylate_cyc; 1.
 DR SMART; SM00044; CYCC; 1.
 DR PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.
 DR PROSITE; PS00125; GUANYLATE_CYCLASES_2; 1.
 KW lyase.
 SQ SEQUENCE 600 AA; 68099 MW; 7FD0136E6ADACB9 CRC64;

Query Match 58.9%; Score 1903.5; DB 5; Length 600;
 Best Local Similarity 60.3%; Pred. No. 2.1e-135;
 Matches 366; Conservative 94; Mismatches 138; Indels 9; Gaps 4;

1 MGFVNAHELELVIRNYGPEWEDIKKKAQDEEGFLVRIYDSKTYDLVAASKVYN 60
 1 MGFVNAHELELVIRNYGPEWEDIKKKAQDEEGFLVRIYDSKTYDLVAASKVYN 60
 1 MGFVNAHELELVIRNYGPEWEDIKKKAQDEEGFLVRIYDSKTYDLVAASKVYN 60
 1 MGFVNAHELELVIRNYGPEWEDIKKKAQDEEGFLVRIYDSKTYDLVAASKVYN 60
 61 IDAGDILQFGKMFEEFCQESGYDTLIRVLSNVREFLQNDLHDLHGLTIYGMKAPSP 120
 61 IDAGDILQFGKMFEEFCQESGYDTLIRVLSNVREFLQNDLHDLHGLTIYGMKAPSP 120
 61 IDAGDILQFGKMFEEFCQESGYDTLIRVLSNVREFLQNDLHDLHGLTIYGMKAPSP 120
 61 IDAGDILQFGKMFEEFCQESGYDTLIRVLSNVREFLQNDLHDLHGLTIYGMKAPSP 120
 121 RCTDAEKKGKGLLHYHSEREGLODIYIGIKTYAAQIHGTEIDMKYIOORNECDHTOFL 180
 121 RCTDAEKKGKGLLHYHSEREGLODIYIGIKTYAAQIHGTEIDMKYIOORNECDHTOFL 180
 121 RCTDAEKKGKGLLHYHSEREGLODIYIGIKTYAAQIHGTEIDMKYIOORNECDHTOFL 180
 121 RCTDAEKKGKGLLHYHSEREGLODIYIGIKTYAAQIHGTEIDMKYIOORNECDHTOFL 180
 181 IEKSKEDFEYDLDREFENGQESRISPYTFCKAFPHIIFDRDLVYTOGNAIYRYL 240
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 181 IEKSKEDFEYDLDREFENGQESRISPYTFCKAFPHIIFDRDLVYTOGNAIYRYL 240
 181 IEKSKEDFEYDLDREFENGQESRISPYTFCKAFPHIIFDRDLVYTOGNAIYRYL 240
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 241 POLQPCNSLVSFSLVRPHIDISFGILSHINTVFLSKEGLDVKECEDELGTGE 300
 241 POLQPCNSLVSFSLVRPHIDISFGILSHINTVFLSKEGLDVKECEDELGTGE 300
 241 POLQPCNSLVSFSLVRPHIDISFGILSHINTVFLSKEGLDVKECEDELGTGE 300
 301 ISCLRKGOMIYLPKADSLIFLCSPSVMNLDLTRGLYLSIDPLDARFDVLLGEQFR 360
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 301 ISCLRKGOMIYLPKADSLIFLCSPSVMNLDLTRGLYLSIDPLDARFDVLLGEQFR 360
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 361 EEYKLTQELIETDLRQLTLRALDEKKKTDTLLYSVLPPSVANELRHRPVPARYKDY 420
 361 EEYKLTQELIETDLRQLTLRALDEKKKTDTLLYSVLPPSVANELRHRPVPARYKDY 420
 361 EEYKLTQELIETDLRQLTLRALDEKKKTDTLLYSVLPPSVANELRHRPVPARYKDY 420
 361 EEYKLTQELIETDLRQLTLRALDEKKKTDTLLYSVLPPSVANELRHRPVPARYKDY 420
 421 TILFSGIVGFNAFCSKHASGEGAMKIVNLNDLYTRFDLTDSKKNPFYKYVGVGDKYM 480
 421 TILFSGIVGFNAFCSKHASGEGAMKIVNLNDLYTRFDLTDSKKNPFYKYVGVGDKYM 480
 421 TILFSGIVGFNAFCSKHASGEGAMKIVNLNDLYTRFDLTDSKKNPFYKYVGVGDKYM 480
 421 TILFSGIVGFNAFCSKHASGEGAMKIVNLNDLYTRFDLTDSKKNPFYKYVGVGDKYM 480
 481 TVSGILPEPCIHARSICHLADMMETAGOVQVDSGVOITIGITHEVYTVGVIGQMPRY 540
 481 TVSGILPEPCIHARSICHLADMMETAGOVQVDSGVOITIGITHEVYTVGVIGQMPRY 540
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 541 CLFGNTVNLTSRTEETGEGKINVSRYTYRCLMSPNSDPOFLHREGVSMKGKREPMO 600
 541 CLFGNTVNLTSRTEETGEGKINVSRYTYRCLMSPNSDPOFLHREGVSMKGKREPMO 600
 541 CLFGNTVNLTSRTEETGEGKINVSRYTYRCLMSPNSDPOFLHREGVSMKGKREPMO 600
 541 CLFGNTVNLTSRTEETGEGKINVSRYTYRCLMSPNSDPOFLHREGVSMKGKREPMO 600
 601 VWFLSRKNP 609
 601 VWFLSRKNP 609
 601 VWFLSRKNP 609
 601 VWFLSRKNP 609

Db	532	CLFGNTVVLFRCEFTTGPVGTINVSEDTYNTLMREDNHDEQPELTLYRGHVTWKGAEPHQ	591
QY	601	VWFLSRK 607	
Db	592	TWFLTRK 598	
RESULT 5			
ID	Q24086	PRELIMINARY:	PRT: 758 AA.
AC	Q24086		
DT	01-NOV-1996	(TREMBLrel. 01, Created)	
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)	
DT	01-MAR-2002	(TREMBLrel. 20, Last annotation update)	
DE	Soluble guanylyl cyclase beta subunit.		
GN	GYC-BETA-100B OR DGCB1 OR CG1470.		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Insecta; Hexapoda; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7227;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=OREGON-R;		
RX	MEDLINE=95318108; Pubmed=7797526;		
RA	Shah S., Hyde D.R.;		
RT	"Two Drosophila genes that encode the alpha and beta subunits of the		
RL	brain soluble guanylyl cyclase.";		
DR	J. Biol. Chem. 270:15368-15376(1995).		
DR	EMBL: U27123; AAA87941.1; -.		
DR	HSSP; P16068; 1AMN.		
DR	FLYbase; FBgn0013973; Gyc-beta-100B.		
DR	InterPro; IPR001054; G_cyclase.		
DR	Pfam; PF00211; guanylate_cyc; 1.		
DR	SMART; SM00044; CYCC; 1.		
DR	PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.		
DR	PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.		
KW	lyase.		
SW	SEQUENCE 758 AA; 84444 MW; FBIDC388142EEF09 CRC64;		
Query Match 58.3%; Score 1883; DB 5; Length 758;			
Best Local Similarity 49.9%; Pred. No. 1e-133;			
Matches 371; Conservative 102; Mismatches 125; Indels 146; Gaps 7;			
QY	1	MYGVNNALELVIRNNGPEVEMEDIKKRAQDDEGQFLVRIITDSDKYIDVLAASKVLN 60	
Db	1	MYGVNNALELVIRNNGPEVEMEDIKKRAQDDEGQFLVRIITDSDKYIDVLAASKVLN 60	
QY	61	LNAGEIITOMEGKMEFVFCQESGYDTILRLVLSNVNEFLQNTDALDHDLATITPGKRAPSF 120	
Db	61	IPADDIIELEKFEFFECQDGSQGYKIIQVGLATPRDFIQNDLALDHDLGTLTPGKRAPSF 120	
QY	121	RCTDAEKGKGLIHYISERESGLQDIVIGIITVAAQIHGTEIDMKVIOORNE----- 172	
Db	121	RCT--EKDGLLHYISERPEGLIEHIVIGIVAAVASKLGVHEIDIVYKRKEPIDAEAKE 178	
QY	173	----- 172	
Db	179	RAIARENQQLLEDVAVATTTSATVVLAPSSDAERNNHNSNGSNNGMANGNTVAVN 238	
QY	173	-----EC-----DHTQFLIE 182	
Db	239	NNNDGQIASETDSIALSTFCPIADSPDCDCKGEQKCLRLKKKSSDIERYDHYQLIR 298	
QY	183	E-----KSKREDYEDDRREENGQTQSRISPTIFCAAPPHIIFDDLVYVYQGN 234	
Db	299	EINVAASKQVADKDEVPDDMEFL---CEAPLISPAFCVCFPPHMLFDRQMKIVQAGK 354	
QY	235	AIYVAFPOLQNGNSLVSFSLVAPPHIDISPHGISHSNTYFVLSRSGKLGDVERKECD 294	
Db	355	AVSNVIRVAAEENKSLIEVVAIRPHQIANTENISHTNTIYVLTQTRGAMS----- 406	
QY	295	ELVGTETSCRLKGMQIYLPKADSIPLFCSPVNNLDDLTRRGILYSLDIPLDATRDIVL 354	

Db	407	--SRHQDRFLRLKGGMMYIPEDRILLFCQCYPMALDLITKGLTISVPLMDARLVL	464
Oy	355	LGQFREKRYLQGELEILTDRLQTLRALADEKRTTLLYSVLPVSANELRRKRPVA	414
Db	465	LSKFEAFEYKLTATNMLTNDKTLQGFREJFRODSEKQXTDRILTSVLPKSVANELRHQRPVP	524
Oy	415	KRDQNTYILFSGIVGNCMSKHAHSGEAMKIVNLTNDLTYREPTLDNRKPNFYVER	474
Db	525	KRTDSYTLFMSGIVGGOYCAANTDPDGMKIVKKNLNTLYVFDALDTSKRNKNLVYVER	564
Oy	475	VGDKRYMTVSGLPERCIHHRASICHALDMMELTAGOVYDGSVSQITIGIHGEVYTVIG	534
Db	585	VGDKRYMAVSGLPDHCEDHAKCAKVARLDMQAKNVKGSNPVQITIGIHGEVYTVIG	644
Oy	535	QRMPRCILFQNTYVNLSTRTEYTGKIKVINSYTRCLMSPEKSDPQHLERHPVSMKG	594
Db	645	NRPVRCILFQNTYVNLSTRTEYTGVPVRINVSERYRLCMAIINDDSFHLERYKQPVIMKG	704
Oy	595	KKEPMQWFLSRKNT---GTEET 614	
Db	705	KPPMCMQWFLSTRATSSILGTSST 728	
RESULT 6			
O9VA09			
O9VA09		PRELIMINARY;	PRT; 787 AA.
AC	O9VA09		
DT	01-MAY-2000	(TEMBLrel. 13, Created)	
DT	01-MAY-2000	(TEMBLrel. 13, Last sequence update)	
DT	01-MAY-2002	(TEMBLrel. 20, Last annotation update)	
DE	GyCBETA100B	protein.	
GN	GyC-BETA-100B	OR GyCBETA100B OR CG1470.	
OS	Drosophila melanogaster	(Fruit fly).	
OC	Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:		
OC	Pterygota: Neoptera: Endopterygota: Diptera: Blatthycera; Muscomorpha;		
OC	Ephydroidea: Drosophilidae; Drosophila.		
OX	NCBI_taxid=7227;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-BERKELEY.		
RX	MEDLINE-20196006; PubMed-10731132;		
RA	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RA	Amaratilaka P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,		
RA	George R.A., Lewis S.E., Richards S., Ashburner K., Henderson S.N.,		
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,		
RA	Brandon R.C., Rogers J.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,		
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,		
RA	Abriil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,		
RA	Ballew R.M., Basu A., Baxendale J., Bayraktarglu L., Beasley E.M.,		
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,		
RA	Botkova D., Botchan M.R., Bouck J., Brokstein P., Brotcler P.,		
RA	Burtis K.C., Busam D.A., Butler H., Cadieu L.B., Cantler A., Chandra I.,		
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,		
RA	de Palcos B., Delcher A.A., Deng Z., Mays A.D., Dew I., Dietz S.M.,		
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,		
RA	Durbin K.J., Evangelista C.C., Ferraz C., Periera S., Fleischmann W.,		
RA	Foster C., Gabriellian A.E., Garg N.S., Gelbart W.N., Glasser K.,		
RA	Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,		
RA	Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,		
RA	Hoskins R., Houston K.A., Howland T.J., Wei M.-H., Idbegun J.,		
RA	Jamali M., Kalush F., Kapran G.H., Ke Z., Kennison J.A., Ketchum K.A.,		
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,		
RA	Lasko P., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,		
RA	Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,		
RA	Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,		
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,		
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Peclab J.M.,		
RA	Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,		
RA	Reinelt K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,		
RA	Shue B.C., Siden Klamos I., Simpson M., Skupski M.P., Smith T.,		
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,		
RA	Stavitskaya R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,		

RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveril J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000).
 DR EMBL: AB003777; AAF57119.1; -.
 DR HSP; P16068; 1ANN.
 DR F1ybase; Fgpn0013973; Gyc-beta-100B.
 DR InterPro; IPR001054; G_cyclase.
 DR Pfam; PF00211; guanylate_cyc; 1.
 DR SMART; SM00044; CYC; 1.
 DR PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.
 DR PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
 KW Lyase.
 SQ SEQUENCE 787 AA; 86849 MW; ABD2F4B6D09C72B8 CRC64;

 Query Match 58.3%; Score 1883; DB 5; Length 787;
 Best Local Similarity 49.9%; Pred. No. 1.1e-133;
 Matches 371; Conservative 102; Mismatches 125; Indels 146; Gaps 7;

 QY 1 MGFVNHAELELVIRNYGPEWEDIRKEAQLDEGOLFRIITYDSKTYDLVAASKVYN 60
 DB 1 MGFVNHAELELVIRNYGPEWEDIRKEAQLDEGOLFRIITYDSKTYDLVAASKVYN 60
 QY 61 INAGETLQMGKMFVFCOESGYDTLRLVGSNVEFLQNLALHDLHATYPGMRAPSF 120
 DB 61 IPADLLELFKGTFFECODSGYDKLQYLQATPRFLQNLALHDLHATYPGMRAPSF 120
 QY 121 RCTDAEKKGGLIHYSEREGLODIYIGIKTYAQQIHGETIDMKYIQORNE----- 172
 DB 121 RCT--EKDGEILLHYSERGLEHIVYIGVAKVASKLHGEVEIDIVKKEPIDAEKE 178
 QY 173 ----- 172
 DB 179 RALAEHQQLLEDVAATTGTSATVYVLAPSSDAERNNNHNGSNNNGMANNGTAVN 238
 QY 173 -----BC-----DHQFLIE 182
 DB 239 NNNDGQIASETDPSIALSTCPILAQSPFCDDGDKQKCLRLKNSKSDIERDHYQFLIR 298
 QY 183 E-----KESKEDFYDDLRFENGNGQESRISYTTCKAPPHIITDRDLVYQCGN 234
 DB 299 EINVAAKSGVDAKKEVPDMEFL-----CEAPLISPATFCVPPFLMEDRQKIVQAGK 354
 QY 235 AIVRYLPOLQPCNCLSVFSLYVRPHIDISFGIISHINTVFLRSKGLDVEKLECD 294
 DB 355 AYSRIYPRAEKNCSTIEVEAIRPHLOINTEINILSHINTIYVLOTROGAMS----- 406
 QY 295 ELTGTEISCLRLKGOMIYLPBADSILFLCSPVNMIDLTRGLYSLDIPLDATRDLYL 354
 DB 407 --SRHEQRLRLKGMVYIPEDRIILFCYPSVNMIDLTRKGLYSDVPLHDAARDLYL 464
 QY 355 LGEQREEEKLQOELEILTDRLQTLRALEDEKKTDITLSTVPSVANELRHRPVA 414
 DB 465 LSEKEAEKRLKKNLEMLTDKLOQTFRDESEKQKDRLLYSVLPKSVANELRHRPVP 524
 QY 415 KRYDNTILFSGIVGFNFCSHAGSEGAMKIVNLLNDLYTRFDLTDSKKNPFYKVE 474
 DB 525 KRYDSTILFSGIVGGOYCAANTDPDGMKIVKMLNELTYFDALTDSCRNLNAYKVE 564
 QY 475 VQDKTYWVSGLEPDCIHHARSICHLALDMMETIAGOVODGESVQITIGIHGEVTVG 534
 DB 585 VQDKTYWVSGLEPDCIHHARSICHLALDMMETIAGOVODGESVQITIGIHGEVTVG 644
 QY 535 QMRPRCLEGNTVNLSTRETGEGKINVSSETTYCMLSPENDSQPHLEHGPVSAMG 594
 DB 645 NNPVRCLEGNVTNLSRTETGVPGRINVSSETTYRLCMAINQDSDSFLLEYRGMVG 704
 QY 595 KKEPMQVFLSKRNT-----GTEET 614
 DB 705 KPLPDMCWLTRATSSILGTSSIT 728

RESULT 7
 Q95NK5 PRELIMINARY; PRT; 604 AA.
 AC Q95NK5;
 DT 01-DEC-2001 (TREMBLrel, 19, Created)
 DT 01-DEC-2001 (TREMBLrel, 19, last sequence update)
 DT 01-MAR-2002 (TREMBLrel, 20, last annotation update)
 DE Soluble guanylyl cyclase beta1.
 GN HPGCS-BETA1.
 OS Hemileictrous pulcherrimus (Sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidae; Euechinoidae; Echinacea; Echinoida; Strongylocentrotidae;
 OC Hemileictrous.
 OX NCBI_TaxId=7650;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tanabe Y., Suzuki N.;
 RT "Genomic Structure and Expression of the Sea Urchin Soluble Guanylyl
 RT Cyclase beta Subunit Genes."
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB062390; BAB58877.1; -.
 DR EMBL: AB062387; BAB58877.1; JOINED.
 DR EMBL: AB062388; BAB58877.1; JOINED.
 DR EMBL: AB062389; BAB58877.1; JOINED.
 DR EMBL: AB062386; BAB56135.1; -.
 DR InterPro; IPR001054; G_cyclase.
 DR Pfam; PF00211; guanylate_cyc; 1.
 DR PROSITE; PS00452; GUANYLATE_CYCLASES_1; UNKNOWN.1.
 DR PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
 SQ SEQUENCE 604 AA; 68198 MW; B1C79618705934D2 CRC64;

 Query Match 57.9%; Score 1870.5; DB 5; Length 604;
 Best Local Similarity 57.2%; Pred. No. 6.7e-133;
 Matches 351; Conservative 112; Mismatches 126; Indels 25; Gaps 5;

 QY 1 MGFVNHAELELVIRNYGPEWEDIRKEAQLDEGOLFRIITYDSKTYDLVAASKVYN 60
 DB 1 MGFVNHAELELVIRNYGPEWEDIRKEAQLDEGOLFRIITYDSKTYDLVAASKVYN 60
 QY 61 INAGETLQMGKMFVFCOESGYDTLRLVGSNVEFLQNLALHDLHATYPGMRAPSF 120
 DB 61 ISANDLLEAFGRFFECVSGSDNTLNLVGSYTRFLQNLALHDLHATYPGMRAPSF 120
 QY 121 RCTDAEKKGGLIHYSEREGLODIYIGIKTYAQQIHGETIDMKYIQORNE----- 180
 DB 121 RCTRSDDALVHYHSERGLEHIVYIGVRSYAKTLHSEVVEITKNGECDAHYORA 180
 QY 181 IEKSKEDFYEDDLRFENGTO-----ESRISPYTCKAPPHIIFDRDLVYQCG 233
 DB 181 IIEK-----VETAKIEKQARONLALSKKPKISPTLCRIILPHINMELNVEQNG 232
 QY 234 NATRYLPOLQPCNCLSVFSLYVRPHIDISFGIISHINTVAVLSKGLDVEKLEB 293
 DB 233 NSIQRIIVPININNCMTDLFHYVRPHMETFFSILSHANTIVLTNGSVN-----P 286
 QY 294 DELTGTEISCLRLKGOMIYLPBADSILFLCSPVNMIDLTRGLYSLDIPLDATRDLY 353
 DB 287 NNPVRCLEGNVTNLSRTETGVPGRINVSSETTYRLCMAINQDSDSFLLEYRGMVG 346
 QY 354 LGEQREEEKLQOELEILTDRLQTLRALEDEKKTDITLSTVPSVANELRHRPVP 413
 DB 347 LISERDEEEKLQOELEILTDKLOQYRREIENKKKTDRLYSLPVSANELRHRPVP 406
 QY 414 AKRYDNTILFSGIVGFNFCSHAGSEGAMKIVNLLNDLYTRFDLTDSKKNPFYKVE 473
 DB 407 AKKECVTLTFSGISFEGFCRRYS--HDMKIVSLNSVYTKFEDVLMEN--NPDYKVE 462
 QY 474 TVGDKTYWVSGLEPDCIHHARSICHLALDMMETIAGOVODGESVQITIGIHGEVTVG 533
 DB 463 TVGDKTYWVSGLEPDCADHAKCIKAKMALEKKEKLSADYINMGGDVIITIGVSGEVTVG 522

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OY 534 GORPRCLGNYVNTLSRTETGKRVSEYTYRCLSPNSDPQHLEHNGVSMK 593
DB 523 GORPRCLGNYVNTLSRTETGKRVSEYTYRCLSPNSDPQHLEHNGVSMK 582
OY 594 GKRPQWFLSRK 607
DB 583 GKRPQWFLSRK 596

RESULT 8
OY 017010 PRELIMINARY: PRT: 649 AA.
DB 017010: 017007; 017008; 017009;
AC 017010; 017007; 017008; 017009;
DB 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Soluble guanylyl cyclase beta subunit (Fragment).
GN GCSBERA.
OC Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
OC Anopheles.
OX NCBI_TaxID=7165;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SUA;
RX MEDLINE=99124361; Pubmed=9927171;
RA Caccione A., Garcia B.A., Mathiopoulos K.D., Min G.S., Moriyama E.N.,
RA Powell J.R.;
RT "Characterization of the soluble guanylyl cyclase beta-subunit gene in
RT the mosquito Anopheles gambiae."
RL Insect Mol. Biol. 8:23-30(1999).
RN [2]
RP SEQUENCE OF 539-649 FROM N.A.
RC STRAIN-SUA, G3, GMMKG, AND MD;
RX MEDLINE=96400927; Pubmed=8807303;
RA Garcia B.A., Caccione A., Mathiopoulos K.D., Powell J.R.;
RT "Inversion monophyly in African anopheline malaria vectors."
RT Genetics 143:1313-1320(1996).
RL EMBL; U42613; AAC47142.1; -
DR EMBL; AF017062; AAC47144.2; -
DR EMBL; U42612; AAC47141.1; -
DR EMBL; U42614; AAC47143.1; -
DR HSSP: P16068; 1AMN.
DR InterPro: IPR001054; G_cyclase.
DR Pfam: PF00211; guanylate_cyc; 1.
DR SMART; SM00044; CYCC; 1.
DR PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.
DR PROSITE; PSS0125; GUANYLATE_CYCLASES_2; 2.
KM Lyase.
FT NON_TER
SQ SEQUENCE 649 AA; 72514 MW; 376BAC40422C59DB CRC64;

Query Match 54.58; Score 1761; DB 5; Length 649;
Best Local Similarity 52.08; Pred. No. 1.4e-124;
Matches 345; Conservative 94; Mismatches 116; Indels 108; Gaps 4;

OY 2 YGFVNHALLVIRNYPPEWEDIKRKAQDLDESGFLVRIYDSSKTYDLVAASKVLT 61
DB 1 YGFVNHALLVIRNYPPEWEDIKRKAQDLDESGFLVRIYDSSKTYDLVAASKVLT 60
OY 62 NAGEIILQMGKMFVFCQESGYDTILRVGNSVREFLQNDALHDHLATYVPGKRAPSR 121
DB 61 PADDIILELFEKTFEEFCQDSGYDKILQVLTATPDPFLQNDALHDHLATYVPGKRAPSR 120
OY 122 CTDAEKKGKILHYYSRELDIVIGITVAQOIHGTETDMKVIOQRN----- 171
DB 121 CT--ETNGQLVLYHSERPELHVIGIVRAVASKLGVVEIKIIRKGDVPEAKKA 178
OY 172 ----- 171
DB 179 TAEPVANTAAATPKARHSIPEVYKSVPTISLDPANPELANGLCKRIIAKTSSTSGP 238

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OY 172 -----EEDHVFILIE---KSEKEDFYEDLDREENGTOESR 207
DB 239 ARNGPEWQKPKPGPTAVERSDHPQLITTEISGPKTPRRSDENQDAVAVOLVAKEP 298
OY 208 ISPTPKAPFPHIIPDRDLVYQCGNAIRVLQPLQPCNSLISVSLVRPHIDISFHG 267
DB 299 ISPTPKAPFPHIIPDRDLVYQCGNAIRVLQPLQPCNSLISVSLVRPHIDISFHG 358
OY 268 ILSHINTEVYLRKNEGLDVEKLECEDELTGTEISCLRLKGMIVLEADSIPLCSPSV 327
DB 359 ILAHINTEVYLRKNEGLDVEKLECEDELTGTEISCLRLKGMIVLEADSIPLCSPSV 406
OY 328 MNIDLTTRKGLVSLDIPLDHATRDVLVLSQFPEEKRLNGLEITDRQLTRALEDEK 387
DB 407 MNIDLTTRKGLVSLDIPLDHATRDVLVLSQFPEEKRLNGLEITDRQLTRALEDEK 466
OY 388 KRTDILYSLVPSVANELHKKRPVPAKRDNTIFSGIVGNACSKRASEGMAKIV 447
DB 467 OKTRDLTVLPKTVANELHKKRPVPAKRDNTIFSGIVGNACSKRASEGMAKIV 526
OY 448 NLNDLTTRDPLTDSKRNPFYKRVETVGDKNVTSGLPSPCIHARSICHLADMMEIA 507
DB 527 KMLNELTIFDELDSKNSNITKVEYVGDKNVTSGLPSPCIHARSICHLADMMEIA 586
OY 508 GOVQVDSGVQITIGITGVYVGVIGQRPRLCGNYVNTLSRTETGKRVSEY 567
DB 587 KNYMGTEAMKRTIGISHGEVYVGVIGNRPRLCGNYVNTLSRTETGKRVSEY 646
OY 568 TYR 570
DB 647 TYK 649

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RESULT 9
OY 091XJ7 PRELIMINARY: PRT: 742 AA.
DB 091XJ7: 091XJ7;
AC 091XJ7;
DB 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Soluble guanylyl cyclase beta 2 subunit.
GN GUCY1B2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-KIDNEY;
RX MEDLINE=21391941; Pubmed=11406623;
RA Koglin M., Vohse K., Budeus L., Scholz H., Behrends S.;
RT "Nitric Oxide Activates the beta 2 subunit of Soluble Guanylyl Cyclase
RT in the Absence of a Second Subunit."
RT J. Biol. Chem. 276:30737-30743(2001).
RL EMBL; AF004153; AAF86581.1; -
DR InterPro: IPR001054; G_cyclase.
DR Pfam: PF00211; guanylate_cyc; 1.
DR PROSITE; PS00452; GUANYLATE_CYCLASES_1; UNKNOWN_1.
DR PROSITE; PSS0125; GUANYLATE_CYCLASES_2; 1.
SQ SEQUENCE 742 AA; 83050 MW; 41CE148B15E244E4 CRC64;

Query Match 34.28; Score 1105; DB 11; Length 742;
Best Local Similarity 36.98; Pred. No. 6.6e-75;
Matches 249; Conservative 117; Mismatches 221; Indels 88; Gaps 13;

OY 1 MYGFVNHALLVIRNYPPEWEDIKRKAQDLDESGFLVRIYDSSKTYDLVAASKVLT 60
DB 1 MYGFVNHALLVIRNYPPEWEDIKRKAQDLDESGFLVRIYDSSKTYDLVAASKVLT 58
OY 61 LNAEIIQMGKMFVFCQESGYDTILRVGNSVREFLQNDALHDHLATYVPGKRAPSR 120
DB 61 LNAEIIQMGKMFVFCQESGYDTILRVGNSVREFLQNDALHDHLATYVPGKRAPSR 120

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Db 59 VSMELIKLFGYFFKFCMSGYDRMLRTLGNGLEFFINLDALHSYALSTQEMNAPSF 118
Qy 121 RCTDAEKGLILHYSSEREGLDVIIGITKVAQIHGTEIDMKYIOORNEC----- 174
Db 119 RVEEGADG-AMLLHYSDRHGLCHIVPGIIEAVAKFFPTDVAMSLDM-NEEVERTGK 176
Qy 175 DHTOFLIEKESKE-----EDFYED----- 194
Db 177 EHAVELVVOAKHROIGAKASRPOGSEDSQADQALQTLRLMKERYLINIPVCPGKSHS 236
Qy 195 -----LDREENGTOESRISPYTFCKAPFHIIIFRDLYVTQCGNATYRL 240
Db 237 TAVRASVLFKGPPLRDFQPYPERLWEEVEVCDPFIHVFDEALRVKQAGVNIQKY 296
Qy 241 POLQPGNSLSVSLVRPHIDISFGLSHINTVFLRSKEGLDVEKLECEDELGTGE 300
Db 297 PELTQKFAIDYEFSIIHPQVTFNISICKFINSQFVLKTKREMPKAR-----KS 347
Qy 301 ISCLALKGMITLPEADSLIFLCSPSVNMUDLTRGLYLSDIPLDATRDVLLGEOR 360
Db 348 QPMLLRGMIMWESLRCMIFMCSFVNRSLQELLESKMLSDIAPHDTTRDLILNQORL 407
Qy 361 EFKTLQELTLDRLQTLRALDEKKTDTLLYSVLPSPVANELRHRKRPVAKRYDNY 420
Db 408 AMELSCQLEKKEKELRVLSNHLAIKKETETLLYAMLEPHVANOIKRGKVAAGEFTJC 467
Qy 421 TILFSGIVGFNAFCSKSHASGEGAMKIVNLDLYTRFDLTDSRKNPFYKVTVDKYM 480
Db 468 TILFSDVVTFTNIC--AAFC-PIQIVNMLSMYSKFDRLTSVHD--VYKVEITIDAW 520
Qy 481 TVSGLEPCHIHARSICHLADMMELIAGOV--VDGESVQITIGITGVEVTVGIGOR 538
Db 521 YVGAVPVPEASHAQRVANFALGMRSKAKVNPVTGEPIQIRVGITGVLAGVVDKRP 580
Qy 539 RYCLFGNTVNLSTRTTETGKGINVSEYTRCLMSPENDPOFHLHRGPVSMKKEPE 598
Db 581 RYCLGDTVNTASRMSHSLPSKVLHSPFAHRL-----KNGKEIYVRGEIEVKGK 634
Qy 599 KQWFLSRKNTGTE 613
Db 635 MTFYELQNLNATED 649

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RESULT 10

Q92001

PRELIMINARY; PRT; 636 AA.

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AC 092001;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Soluble guanylate cyclase beta 2b.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RA Okamoto H., Asakawa T.;
RT "cDNA cloning and expression analysis of novel variant of rat sgc
RT beta2 subunit.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB058888; BAB68564.1; -
DR InterPro; IPR001054; G_cyclase.
DR Pfam; PF00211; guanylate_cyc; 1.
DR PROSITE; PSS00452; GUANYLATE_CYCLASRS_1; UNKNOWN_1.
DR PROSITE; PSS0125; GUANYLATE_CYCLASRS_2; 1.
SQ SEQUENCE 636 AA; 71642 MW; 931DBD8970E0890 CRC64;

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Query Match 30.4%; Score 983; DB 11; Length 636;
 Best Local Similarity 36.7%; Pred. No. 8.9e-66;
 Matches 224; Conservative 104; Mismatches 196; Indels 86; Gaps 12;

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Qy 66 ILQMGKMEFFVQCSGYDTLLVIGLSNVREFLQNLDAHLATIPQMRAPSFECTDA 125
Db 4 ILKLFGEYFFKFCMSGYDRMLRTLGNGLEFFINLDALHSYALSTQEMNAPSFVEEG 63
Qy 126 EKGKGLILHYSSEREGLDVIIGITKVAQIHGTEIDMKYIOORNEC-----DHTOP 179
Db 64 ADG-AMLLHYSDRHGLCHIVPGIIEAVAKFDPDVAMSLDM-NEEVERTGKKEHYVF 121
Qy 180 LIBEKESKE-----EDFYED----- 194
Db 122 LVYQKHRHROIGAKASRPOGSEDSQADQALQTLRLMKERYLINIPVCPGKSHS 181
Qy 195 -----LDREENGTOESRISPYTFCKAPFHIIIFRDLYVTQCGNATYRLPOLP 245
Db 182 SVLFKGPPLRDFQPYPERLWEEVEVCDPFIHVFDEALRVKQAGVNIQYVGILT 241
Qy 246 GNSLSVSLVRPHIDISFGLSHINTVFLRSKEGLDVEKLECEDELGTETLSCL 305
Db 242 QKFAIDYEFSIIHPQVTFNISICKFINSQFVLKTKREMPKAR-----KSOPMLK 292
Qy 306 LKGMITLPEADSLIFLCSPSVNMUDLTRGLYLSDIPLDATRDVLLGEORREYKL 365
Db 293 LRQGMIMWESLRCMIFMCSFVNRSLQELLESKMLSDIAPHDTTRDLILNQORLAMEL 352
Qy 366 TQELTLDRLQTLRALDEKKTDTLLYSVLPSPVANELRHRKRPVAKRYDNYTLFS 425
Db 353 SCQLEKKEKELRVLSNHLAIKKETETLLYAMLEPHVANOIKRGKVAAGEFTCTILPS 412
Qy 426 GIYGFNAFCSKSHASGEGAMKIVNLDLYTRFDLTDSRKNPFYKVTVDKYMVSG 485
Db 413 DVVTFTNIC--AAFC-PIQIVNMLSMYSKFDRLTSVHD--VYKVEITIDAWVVG 465
Qy 486 PEPCIHARSICHLADMMELIAGOV--VDGESVQITIGITGVEVTVGIGORPRYCL 543
Db 466 PVVESHARVANFALGMRSKAKVNPVTGEPIQIRVGITGVLAGVVDKRPYCLF 525
Qy 544 GNTVNTSTRTTETGKGINVSEYTRCLMSPENDPOFHLHRGPVSMKKEPEQW 603
Db 526 GDTVNTASRMSHSLPSKVLHSPFAHRL-----KNGKEIYVRGEIEVKGK-MTFY 579
Qy 604 LSRKNTGTE 613
Db 580 LTQNLNATED 589

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RESULT 11

Q9XTE0

PRELIMINARY; PRT; 685 AA.

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AC 09XTE0;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE C46E1.2 protein.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodieridae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Atkinson R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Dutilleul R., Favell A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kerhaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Ritken L., Roopra A., Saunders D., Shownkeen R.,
RA Shalton N., Smith A., Sonhammer E., Staden R., Sulston J.,

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QY 491 HHARSICHLALDMMELIAGOVQ--VDGESVQITIGIHTEGVTVIGVIGORMPRYCLFGNTVN 548
DB 518 EHAEMCHVALGMMEARSVMDPVNKTPLRLIGHSGITLIGVYGTGKMPRCCLGEYAT 577
QY 549 LTRFETGEKGINVSETTYRCCLMSPENDPOFLEHNGPVSMMGKKEPMQWFLSR-- 606
DB 578 LASOMESLGAVKRICQSSWTY---SKAMETGFEFSPRGRIINVGRGD-VETFTLMBSL 632
QY 607 KNTGTEETKODD 619
DB 633 KKSWEITDHERD 645

RESULT 13
ID 076340 PRELIMINARY; PRT: 940 AA.
AC 076340:
DB 01-NOV-1998 (TREMBLrel. 08, Created)
DB 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DB 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Soluble guanylyl cyclase beta-3.
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditylaria;
OC Sphingioidea; Sphingidae; Sphinginae; Manduca.
OX NCBI_Taxid=7130;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99107914; PubMed=9891024;
RA Nighorn A., Byrnes K.A., Morton D.B.;
RT "Identification and characterization of a novel beta subunit of
RT soluble guanylyl cyclase that is active in the absence of a second
RT subunit and is relatively insensitive to nitric oxide.";
RL J. Biol. Chem. 274:2525-2531(1999).
DR EMBL: AF064514; AAD09836.1;
DR HSSP: Q02846; IAWL.
DR InterPro: IPR001525; C5_DNA_meth.
DR InterPro: IPR001054; G_cyclase.
DR InterPro: IPR001230; Prenyl_site.
DR Pfam: PF00211; guanylate_cyc; 1.
DR SMART: SM00044; CYCC; 1.
DR PROSITE: PS00095; C5_MTASE_2; UNKNOWN_1.
DR PROSITE: PS50125; GUANYLATE_CYCLASES_2; 1.
DR PROSITE: PS00294; PRENYLATION; UNKNOWN_1.
SQ SEQUENCE 940 AA; 106393 MW; 0895686667BD0F6 CRC64;

Query Match 29.6%; Score 955; DB 5; Length 940;
Best Local Similarity 35.1%; Pred. No. 2e-63;
Matches 221; Conservative 123; Mismatches 234; Indels 52; Gaps 13;

QY 1 MTFVNAHLELIVINYPGEVWEDIKKEAQLDEGQFLVRIYDSDKTYDLVAASKVYN 60
DB 1 MTFGLLENNAEYIRQTYGERMEDIRQGV--EQPSFVHOYPPENLIRLAKKQEVUG 59
QY 61 LNAGETLQMGKMFVFCQESGYDTLLRVLSNVREQLNDLALHDHLLATTPGMRAPSF 120
DB 60 IITERFQMGMVYFVGFSQYGYDRLSVLGRHMRDLNGLNHLREYLFKSPRMRAPSF 119
QY 121 RCTDEKKGGLLHYTSEREGLODIVIGIKTYAQQIHTEIDMKYIQOR----- 170
DB 120 IC-EMETRGGLTLHRSKRGRGVYAMGQIREVAFRIYKEMKIELRELLFDTVHVF 178
QY 171 NEECHTOFLIEKESKEDFEYEDLRFENGTOESRIPTYECKAFPHIIFDRDLVYT 230
DB 179 QLTFFNRATFLASLMTREE-----KHLPIASVLELFPPCIYFGSMVVR 225
QY 231 QCGNATIRVLPOLQPGNCSLSVSLVRPHIDISFHHGILSHNTVFLRSKGLDY--- 287
DB 226 SIGNSLMTIPLDV--GKRTIWMFDLVRPLIAFKFQTIINRTNIFELVYVEAVMEKAP 283
QY 288 ----ETLCEDELTGTEISCLRLKGMITLPEADSLIFLCSPSVNMLDLTLRGTLSDI 343

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DB 284 DKRNELLRLSDETDCTEKKENLRLKGMITYMNMRRMMTLGTPVMDLSALVSTGYINDL 343
QY 344 PLHDAITRDVLVLGEQFREFREYKLTQELE--ILTDRLOUTLALBDEKKPTDILLYSPSY 402
DB 344 SKHDSRDLMLAGTQOVSBLKIALDOEQKSKLSESMKRLDEKRRIDELLYOMIPKOV 403
QY 403 ANELBH--KRPV--PARRYDNTILFSGIVGFNAFCSHASGEGAMKIYNLNDLYRFDPL 460
DB 404 ADLRNGENPIDTCEMFDSVSLFSDVYFTEICSRIT---PMEVSLNMYSLIFDPL 459
QY 461 TDSKKNPFYKYETVDKRWYVSGULPERCIHARSICHLALDMMELIAGOVQ--VDGESVQ 518
DB 460 TERNR--YYKVTIGDAMYVVSAGAPERKEDNAEYCDALMDVATIDLPSTGSHLS 516
QY 519 ITIGIHTEGVTVIGVIGORMPRYCLFGNTVNLTSTRTTEGKGINVSETTYRCCLMSPENS 578
DB 517 IYGVHSGAVVAGIYGLKMPRCCLGDSVNTASRHESTSEAKRIHISQTTQELL----- 570
QY 579 DPQFLEHNGPVSMMGKKEPMQWFLSRKN 608
DB 571 SPYMYTERGEIQVGKGMKTYWLEGRS 600

RESULT 14
ID 002298 PRELIMINARY; PRT: 751 AA.
AC 002298:
DB 01-JUL-1997 (TREMBLrel. 04, Created)
DB 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DB 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE T04D3.4 protein.
GN T04D3.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA Kershaw J.K.;
RT Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL: Z81114; CAB03288.1; -.
DR HSSP: P19687; IAWN.
DR InterPro: IPR001054; G_cyclase.
DR InterPro: IPR001230; Prenyl_site.
DR Pfam: PF00211; guanylate_cyc; 1.
DR SMART: SM00044; CYCC; 1.
DR PROSITE: PS00452; GUANYLATE_CYCLASES_1; 1.
DR PROSITE: PS50125; GUANYLATE_CYCLASES_2; 1.
DR PROSITE: PS00294; PRENYLATION; UNKNOWN_1.
SQ SEQUENCE 751 AA; 85380 MW; BC864A0A1A589CE9 CRC64;

Query Match 29.0%; Score 938; DB 5; Length 751;
Best Local Similarity 35.0%; Pred. No. 2.8e-62;
Matches 220; Conservative 125; Mismatches 236; Indels 48; Gaps 15;

QY 1 MTFVNAHLELIVINYPGEVWEDIKKEAQLDEGQFLVRIYDSDKTYDLVAASKVYN 60
DB 1 MCGWIHESRQVLTTRKTYGADIMKTYHMSKFEIGTSETLAHYINDDETILRVNSMANVIG 60
QY 61 LNAGETLQMGKMFVFCQESGYDTLLRVLSNVREQLNDLAL--DHLATY--PGMR 116
DB 61 IPIEBIWEAYGFLIOFTMETGMDLRLAMPADLBEGLDLSLSDLHVFIDHV--VYTKLR 118
QY 117 APSFRCTDAEKKGGLLHYTSEREGLODIVIGIKTYAQQIHTEIDMKYIQORNECP- 175

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Db 119 GPRRC-DVQADGTLHHTYKSKSLPIYKGVREARRYDTEVNVKQERQEHDA 177
 QY 176 -----HTQFLIEEK-----SKEDEYEDIDREENGTOQSRIPTYFCRAPHFI 221
 Db 178 FVTEHVEVATIQIENANSTQPSKISSKADSQLD-----SGIYE-1SSSPSLAFYHI 231
 QY 222 IFPRDLVYTCGNAIYVLPOLQPGNCSLSVSLVRPHIDISFGLSHINTVYLRSK 281
 Db 232 CFPEDLVEHFGNFIRKTFPNAMQERVVDLLELVHVEVPEFSYSEKIKYKNSLFEVRLK 291
 QY 282 EGLDVKLBCEDELGTETISCLRLKGOMIYLPBADSLIFLCSVNMNDLITRGLYLS 341
 Db 292 -GLADIY-----HNANDEAKTYLLKSNMFIIDEKTLIKLVSNNVTRFLIRNHLIS 344
 QY 342 DIPLDATRDVLYLGEQFREBYKLTQLELITDRLQTLRALDEKKTDTLYLSVLP 401
 Db 345 DMQHNDCTRDVIMNOSRMSQVELNRTLEETTKTKMAQELIEKQDTLCELMPAS 404
 QY 402 VANELIRKRPVPKARYNVTILFSGIYGFNAFCSKHSGEGAMKIVNLNDLYRFDLT 461
 Db 405 VADLRSGKAMDAKFAEDCTLLFDYITFNICAMCTPYD---VATLLNDLYLRFLV 460
 QY 462 DSRKNPVYKVEYVDKVTWVSGLPFCIHARSICHLADMELAGOV--QVDESVQI 519
 Db 461 GLHD---AKVETIGDAMYTVGVPKENCENAEVNLISIGMAESKLYLSPITHKPKI 517
 QY 520 TIGIHGEVNTVIGORMPRYCIGNTVNTLSRTETTGKNGKINSEYTYRCLMSPEND 579
 Db 518 RLAVGHCPVAVAGVYGMPCLEGTDTVNVANKMESNGIOCKIHSE---TGKINGLKAN 574
 QY 580 POFLEHGRPVSMKGRKPMQWFLSRKN 608
 Db 575 PSTYFIDRNGTEING-KGMITYFLERND 602

RESULT 15
 QYVECS PRELIMINARY: PRT: 690 AA.
 AC QYVECS;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE CG4154 protein.
 GN CG4154.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_Taxid=7227;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 Adair J.E., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 Baller R.M., Basu A.A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 Borkov D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 de la Pallos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson R., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Rao L.P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 Mekulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon K., Nussken D.R., Paclad J.M.,
 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.-Y., Wasserman D.A., Weissbrock G.M., Weissbach J.,
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gbbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003707; AF55135.1;
 DR HSSP: Q02846; IAWL.
 DR FlyBase: FBgn0038295; CG4154.
 DR InterPro: IPR001525; C5_DNA_meth.
 DR InterPro: IPR001054; G_cyclase.
 DR Pfam: PF00211; guanylate_cyc; 1.
 DR SMART: SM00044; CycC; 1.
 DR PROSITE: PS00095; C5_MTASE_2; UNKNOWN_1.
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 SQ SEQUENCE 690 AA; 78736 MW; 4B736D7413E168AA CRC64;

Query Match 28.8% Score 929.5; DB 5; Length 690;
 Best Local Similarity 34.8%; Pred. No. 1.le-61;
 Matches 218; Conservative 129; Mismatches 231; Indels 49; Gaps 15;

QY 1 MYGFVNALBELVIRNRYGPEWEDIKRKAOLDEBGOPLVRIYDDSKTYDLVAASRYLN 60
 Db 1 MYGILLNLESEYIKSYGEEKMEDIRQAGIDSP-SFVHGVPENLQTLAKAQQVYG 59
 QY 61 LNAEGLIQLNGKMEFFVQESGDTILRVLSNVREFLQNDLHDLATITYGMRAPSF 120
 Db 60 VSESDPMDQMGVYFVGQGYGYRVLSVLRHMRDLNGLNDLHETLKFSYPMRAPS 119
 QY 121 RCTDAEKGKGLIHYBERGLDVIIGIITKVAQOIHGEIMDKVYQOR----- 170
 Db 120 ICENETK-QGLTLIRKSRGRGYTYTIGQIREVARYHHEMHELEEDYVHTF 178
 QY 171 NEECDTQFLIEEKSEKEDFEEDLDPEENGTOQSRIPTYCKAPFIIFDRDLVYT 230
 Db 179 QLFEDNAPFLASLAMPREE-----KHLFISAHVLEIFPCMGVADMYR 225
 QY 231 QCGNAITRVLPOLQPGNCSLSVSLVRPHIDISFGLSHINTVYLRSEGLDVEKL 290
 Db 226 SIGNSLWVILPELL--GKKTAWEDLVRPLIAEFQTLIRKVNNIIFELVVDPTERFDV 283
 QY 291 ECEDEL--TGTE-ISCLRTKGOMIYLPBADSLIFLCSVNMNDLITRGLYLS 346
 Db 284 QNEDLLHDEGSEPEKRLKRGOMVYENKRMLELTPMPDLTSLITGLYINDLSM 343
 QY 347 DATFDVLALGEQFREBYKLTQLELITDRLQTLRALDEKKTDTLYLSVLP 405
 Db 344 DESDMLDLAQOSVELKALDQOQSKSLSEMRDLDEMRKTDLVLQMGIPKQVADR 403
 QY 406 LRR-KRPV-PAKRYDNTILFSGIYGFNAFCSKHSGEGAMKIVNLNDLYRFDLTDS 463
 Db 404 LRRENPIDICEFMDSVSILFSDIVTEISCRIT---PMEVSMINAMYSIFDKLTER 459
 QY 464 RKNPFYKVEYVDKVTWVSGLPFCIHARSICHLADMELAGOV--QVDESVQI 521
 Db 460 NS---YKVEITIGATVAVAGAPDKNHNAREVCMDLVNDVDTLKDSTQHLIRV 516
 QY 522 GHTGGEVNTVIGORMPRYCIGNTVNTLSRTETTGKNGKINSEYTYRCLMSPENDPQ 581
 Db 517 GVHSGAVVAGIVGLKMPRYCLEGTDTVNVANKMESNGIOCKIHSE---KVLIG-----PN 570

OY 582 FHLEHGPVSMGKKKPMQVFLSRKN 608
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Db 571 YKIERGEIDVKGKGTGTWLEEREN 597

Search completed: June 27, 2003, 13:04:43
Job time : 33.2101 secs

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: June 27, 2003, 13:03:32 ; Search time 12.7678 Seconds

(without alignments)
1426.467 Million cell updates/sec

Title: US-09-762-767a-4

Perfect score: 3231
Sequence: 1 MTGFVNAHLELVIRNTPPE.....QVFLSRKNTGTETKQDD 619

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents.AA:*
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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	404	12.5	1075	1	US-07-623-033-2
2	344.5	10.7	1253	4	US-08-864-785-2
3	309.5	9.6	1134	3	US-08-726-214-2
4	309	9.6	533	3	US-08-726-214-18
5	308.5	9.5	1248	3	US-08-726-214-16
6	291.5	9.0	1294	4	US-09-473-717-2
7	291.5	9.0	1305	4	US-08-864-785-3
8	291.5	9.0	1353	3	US-08-894-173-2
9	291.5	9.0	1353	4	US-09-398-193-2
10	291.5	9.0	1353	4	US-09-473-717-3
11	288	8.9	1098	3	US-08-726-214-10
12	286.5	8.9	1144	3	US-08-726-214-6
13	283.5	8.8	1353	4	US-09-398-193-99
14	282.5	8.7	1099	3	US-08-726-214-14
15	282.5	8.7	1168	4	US-09-474-076-2
16	281	8.7	1064	3	US-08-726-214-8
17	280	8.7	1180	3	US-08-726-214-12
18	278.5	8.6	604	4	US-09-008-097-4
19	278.5	8.6	1167	4	US-09-008-097-6
20	278	8.6	1261	4	US-09-473-716-2
21	272.5	8.4	1165	1	US-08-240-357-2
22	271.5	8.4	1090	3	US-08-307-896-3
23	271.5	8.4	1090	3	US-08-726-214-4
24	271.5	8.4	1090	5	PCR-US95-11808-3
25	269.5	8.3	1077	4	US-09-412-210-1
26	252.5	7.8	429	3	US-08-307-896-4
27	252.5	7.8	429	5	PCR-US95-11808-4

28	175.5	5.4	670	2	US-08-997-080-178	Sequence 178, App
29	175.5	5.4	670	2	US-08-997-362-178	Sequence 178, App
30	175.5	5.4	670	4	US-09-095-855-178	Sequence 178, App
31	175.5	5.4	670	4	US-09-324-542-178	Sequence 178, App
32	175.5	5.4	670	4	US-09-205-426-178	Sequence 178, App
33	175.5	5.4	722	2	US-08-997-080-174	Sequence 174, App
34	175.5	5.4	722	2	US-08-997-362-174	Sequence 174, App
35	175.5	5.4	722	4	US-09-095-855-174	Sequence 174, App
36	175.5	5.4	722	4	US-09-324-542-174	Sequence 174, App
37	175.5	5.4	722	4	US-09-205-426-174	Sequence 174, App
38	173	5.4	419	2	US-08-997-080-125	Sequence 125, App
39	173	5.4	419	2	US-08-997-362-125	Sequence 125, App
40	173	5.4	419	4	US-09-095-855-125	Sequence 125, App
41	173	5.4	419	4	US-09-324-542-125	Sequence 125, App
42	173	5.4	419	4	US-09-205-426-125	Sequence 125, App
43	172.5	5.3	112	4	US-08-857-076-75	Sequence 75, App
44	149	4.6	107	4	US-08-857-076-76	Sequence 76, App
45	137.5	4.3	88	3	US-08-894-173-62	Sequence 62, App

ALIGNMENTS

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RESULT 1
US-07-623-033-2
; Sequence 2, Application US/07623033
; Patent No. 5237051
; GENERAL INFORMATION:
; APPLICANT: Garbers, David L.
; APPLICANT: Schultz, Stephanie
; TITLE OF INVENTION: CLONING THE ENTEROTOXIN RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: TITRON, FALLON, LONGMUS & CHESTNUT
; STREET: 100 South Wacker Drive - Suite 960
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60606-4002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/623,033
; FILING DATE: 19901206
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: VU9018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 456-8000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1075 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-623-033-2

Query Match 12.5%; Score 404; DB 1; Length 1075;
Best local Similarity 37.8%; Pred. No. 4.8e-11;
Matches 102; Conservative 40; Mismatches 98; Indels 30; Gaps 8;

QY 354 LAGEPREYKLTQELIITRLQTLRALED-----EKKRTPLTYSVLPSPV 402
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 753 LPHDQKNESY-----MDTLIRRLQTLYSRMLHEHYERTOLYKAEKRDRAHLMPLRLV 807
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QY 403 ANELHKKRPVPAKRYNVNIIISGIVGFNAFCSKHAAGGAMKIVLMDIYTRPTLND 462
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 808 VSLKKEGIVEPELIEVITIFSDIVGFTTIC-KYST---PMEVYMLNDIKYSFDQIVD 863
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Db      HHD---YKVFETIGDNYVAVSGIPMBNGBNRHADVISKMDLIDILSEMGTFLEHLPGJLPW 920
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0Y      ITIGIHTGEVYGVIGORAPRYCLFGNTVNLASRTETTGEGKGINVSEYRYCLMSPENS 578
519
Db      IRIGVHSGCAGVYGVIGIKMPRYCLFEDYNTVNTASRMESTGLPLRIHMSSTIAL--RRT 977
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0Y      DPOFHLEHNGPVMKMGKKEPMQVWFLSRKN 608
579
Db      DQGFLEYRGEVYLYLKGRTETTYNLGMMD 1007
978

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RESULT 2
US-08-864-785-2
Sequence 2, Application US/08864785A
Patent No. 6329566
GENERAL INFORMATION:
APPLICANT: Kaplan, Joshua M.
APPLICANT: Oppenheimer, Allison J.
APPLICANT: Hale, Anne C.
TITLE OF INVENTION: METHODS FOR THE DETECTION, TREATMENT
FILE OF INVENTION: AND PREVENTION OF NEURODEGENERATION
FILE REFERENCE: 00786/353001
CURRENT APPLICATION NUMBER: US/08/864,785A
CURRENT FILING DATE: 1997-05-29
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1253
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-08-864-785-2

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Query Match	10.7%	Score 344.5	DB 4	Length 1253
Best Local Similarity	32.5%	Pred. No. 5.6e-25		
Matches 93, Conservative	45	Mismatches 85	Indels 63	Gaps 8

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Db      239  LARKLELETOCKDHIMISVMPKKVADELKKDAELRRPSANDSCRTSNAAQVODPLA 2398
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OY      407  -----RHKRPVPARKYDNTVTLFSGIVGFNAFCSHASGEGAMKIYNLINDLYTRFDTL 460
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Db      299  KMPVEYRRFRPPTMNLMTNVSTLFIADIAF---TMSSSKSADELVLNLDLFGFRDTL 354
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Db      355  CRLRG---LEKISTGDCIYCAAGCEPDDHACRIYVEGLDITVAIRQPDIDRGQEVNM 411
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OY      520  TIGIHTEGVYVGVIGORMPRYCLFGNTVNLTSRTETTGKGIYNSEYTRCLMS---P 575
         | : : : : : | : : : : : |
Db      412  RVGIITGKVMCMGVGTRKPEFDYFSDNDVILANEMESSGAVRHVSSEATKLLKGYEIE 471
         | : : : : : | : : : : : |
OY      576  ENSDQHFLHNHGPVSM-----GKKRPMQVPL-SRKNGTGE 613
         | : : : : : | : : : : : |
Db      472  EGPD-----YDGLRMVOGQTERRKPRPSMKTFFTKGRINDOVEE 511

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RESULT 3
US-08-726-214-2
Sequence 2, Application US/08726214
Patent No. 6107076
GENERAL INFORMATION:
APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENINYLYL CYCLASE
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433

CITY: Houston
 STATE: Texas
 COUNTRY: United States of America
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.300
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/726,214
 FILING DATE: Concurrently Herewith
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/005,498
 FILING DATE: 04-OCT-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Highlander, Steven L.
 REGISTRATION NUMBER: 37,642
 REFERENCE/DOCKET NUMBER: UTSD:450
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEFAX: (512) 474-7577
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1134 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-726-214-2

Query Match	9.68;	Score 309.5;	DB 3;	Length 1134;
Best Local Similarity	33.18;	Pred. No. 1.5e-21;		
Matches 80;	Conservative 49;	Mismatches 80;	Indels 33;	Gaps 8

```

QY      354  ILGEORREBYKILNOELLITDLOLTALADEKKRDTLIXSLPSSANEUR----- 407
Dp      235  ILMEROKRAFL-QANRCTIEDLR-----LEBENKOKRLMSLIPRVAENKMEDEFLK 288
QY      408  ----HKRPVPAKRYDNTITLPSGIVGFNAFSCSKHASGEMAKIVNLNDLYTRFDTLTD 462
Dp      289  PERIFPK--IYIQRHNVSIILFADIVGFTGLASQCT----AQELVLKLNLELFGFDELAT 342
QY      463  SRKNRPVYVEVYGGCKMYTSGLEPBCJHNASICHLADMMF-----IAGQVYDGSVQ 518
Dp      343  EN---HCRIKIKLGDCTYCVSGSLDTPKTDHNAACVCEWGLMDIDITTSVALETEVD---LN 396
QY      519  ITIGITHEVTVYVIGORAPRYCLRGNTVNLTSRTETTGEGKATINSEYTYRCLMSPENS 578
Dp      397  MRVGLHTGKAVLCGVGLRKMQYDVMNSNDVTILANVMEAGLPGKVHIKTTTLACLINGEY 456
QY      579  DP 580
Dp      457  EP 458

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US-08-726-214-18
Sequence 18, Application US/08726214
Patent No. 6107076
GENERAL INFORMATION:
APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,214
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSD:450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 533 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-726-214-18

Query Match 9.6%; Score 309; DB 3; Length 533;
Best Local Similarity 33.6%; Pred. No. 4,6e-22;
Matches 77; Conservative 45; Mismatches 75; Indels 32; Gaps 7;

QY 367 QLELITRLQTLTALDEKKKDTLLYSVLPSPVANELR-----HKRPVPAK 415
DB 12 QARNCIEDRLR-----LEDENEKORLLMSLIPRVVAMEKEDFLKPERIPHK--IYIQ 64
QY 416 RYDNTLIFSGIVGFNAFCSKASGEAMKIVNLNDLYTRBDTLDSKNPFYKVEIV 475
DB 65 RDNVSTLIFADIVGTGLASQCT---AOELVKLNLLEGFDELATEN---HCRRIKTL 117
QY 476 GDKVTVSGLEPFCIHARSICHLALDME---IAGOVVDESVOITIGIHTEGVYVG 531
DB 118 GDCYCVSGSLQPKNDHACCEMGLMDITISVAENTEVD---LNMKVGILHTGRVLCG 174
QY 532 VIGOMPRICLEGNTVNTLSRTETTGKINVSERYTRCLMSPNSDP 560
DB 175 VGLRKKWQYDWSNDVTLANVMEAGLPCKVHITKTTLACLNGDYEVER 223

RESULT 5

US-08-726-214-16
Sequence 16, Application US/08726214
Patent No. 6107076
GENERAL INFORMATION:
APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENITYL CYCLASE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,214
FILING DATE: Concurrently Herewith

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSD:450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1248 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-726-214-16

Query Match 9.5%; Score 308.5; DB 3; Length 1248;
Best Local Similarity 25.3%; Pred. No. 2,2e-21;
Matches 136; Conservative 86; Mismatches 209; Indels 107; Gaps 22;

QY 153 VAOQIH---GTEIDMKVIOQRNECDHT-----QFLIEEKSEKEDFYED 194
DB 651 LAQALHVOSGPE-----EINKRIEHTIDLSGDKLRREHRIKPSIMKEDSLEIKYSQ 703
QY 195 L--DREENGCT-----QSRISPYFCAFPFHIFDDLVVTOCGNAI 236
DB 704 MDEVFKSLVCAFIYLFETAIQSILSPSSRLMPTI--QESILMLSHALVITTAED- 760
QY 237 YEVLPOLQPGNSLSVSFLVR---PHIDISFGILSHINTVYVLRSEKGLDYEKLE 291
DB 761 YKCLPLILKKTCCWINEFYIARVYIFASILNFGAV--INILMODFQKS--IPLKNLT 816
QY 292 CEDELGTETI-----SCLRLKGQMTYPPADSILFLSPSYM-----NLDDLYTR 336
DB 817 FNSSAFTDICSYPEYFVETGVLANVTCVFL--RLNSVYKLVLLIMIAVALLMETIYA 875
QY 337 GYLSDIPLDHATRD-----LVLLGQFPEEYKIQLELITDRLQTLRA----- 382
DB 876 GLFLSTDNINHGGEFLGKREKSLIMAMFLAVFHGQLE-YRARDPLNRVQAKETI 934
QY 383 --LEDEKKKDTLLYSVLPSPVANEL---RHKRPVPAKRYDNTLIFSGIVGFNAFCSK 436
DB 935 NEMKDLREHNENMLRIILGHVARRFLKEDRDNELYSQSYAVGVAFASIPGPDFYSQ 994
QY 437 HASGEGAKIVNLNDLYTRBDTLDSKNPFYKVEIVGDKMYVSGL--PE--PCIHHA 493
DB 995 TEMNNOGVACRLMEIILADFDLGEEDRFODIEKIKTIGSTYMAVSGSPKQOCEDEKW 1054
QY 494 RSICHLALDMEIAGOVVDGE---SVQITIGIHTEGVYVIGORMPRYCLFGVTNL 549
DB 1055 GHICALADSLALTESIOIKHNSFRNNEFLRIGISGSVAVGIGAKKQYDIWGTAVL 1114
QY 550 TSTRTETTGKINVSERYTRCLMSPNSDPQFHLHRRGVSKKKE---PMQVWFL 604
DB 1115 ASRMDSTGVSGRIQVDEETLYLL---KDGPAFADYREIIVYKISDEGKIKITYFL 1167

RESULT 6

US-09-473-717-2
Sequence 2, Application US/09473717
Patent No. 6372475
GENERAL INFORMATION:
APPLICANT: Storm, Daniel R.
APPLICANT: Hacker, Beth
APPLICANT: Tomlinson, James E.
APPLICANT: COR Therapeutics, Inc.
TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENITYL
CYCLASE
FILE REFERENCE: 44481-5029-01-US

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1 CURRENT APPLICATION NUMBER: US/09/473,717
2 CURRENT FILING DATE: 1999-12-29
3 PRIOR APPLICATION NUMBER: PCV/US98/135411
4 PRIOR FILING DATE: 1998-07-01
5 PRIOR APPLICATION NUMBER: 60/098,559
6 PRIOR FILING DATE: 1997-07-01
7 PRIOR APPLICATION NUMBER: 08/886,440
8 PRIOR FILING DATE: 1997-07-01
9 NUMBER OF SEQ ID NOS: 3
10 SOFTWARE: PatentIn Ver. 2.0
11 SEQ ID NO 2
12 LENGTH: 1294
13 TYPE: PRT
14 ORGANISM: human type IX adenylyl cyclase
15 US-09-473-717-2

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Query Match	9.08;	Score 291.5;	DB 4;	Length 1294;
Best Local Similarity	31.28;	Pred. No. 1.2e-19;		
Matches	74;	Conservative	44;	Mismatches 72;
			Indels	47;
			Gaps	6

[illegible]

```

RESULT 7
US-08-864-785-3
: Sequence 3, Application US/08864785A
: Patent No. 6329566
: GENERAL INFORMATION:
: APPLICANT: Kaplan, Joshua M.
: APPLICANT: Oppenheimer, Allison J.
: APPLICANT: Hart, Anne C.
: TITLE OF INVENTION: METHODS FOR THE DETECTION, TREATMENT
: FILE OF INVENTION: AND PREVENTION OF NEURODEGENERATION
: FILE REFERENCE: 00786/353001
: CURRENT APPLICATION NUMBER: US/08/864,785A
: CURRENT FILING DATE: 1997-05-29
: NUMBER OF SEQ ID NOS: 3
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 3
: LENGTH: 1305
: TYPE: PRT
: ORGANISM: Mus musculus
: US-08-864-785-3

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Query Match	9.08;	Score 291.5;	DB 4;	Length 1305;
Best Local Similarly	31.28;	Pred. No. 1.2e-19;		
Matches 74; Conservative	44;	Mismatches 72;	Indels 47;	Gaps 6;

```

QY 383 EEDKKKTDLLVSLVLPSPVANEL-----RHK----- 409
    ||:::||||:|:::|
Db 323 LEVEKALKERMIHSVMPTIADLMKOGDEESENSYKRAHVSPPKRRKKSIOKAPIAF 382
    ||:::||||:|:::|
QY 410 RPVAKRYRDVNTILFSGIVGENAFCSKHASEGAMKIVNTLNDITYREDTLDSKKNFV 469
    ||:::||||:|:::|:::|:::|:::|:::|:::|
Db 383 RPFMKQOEVSILFADIVGF---TKMSAKMSAHAIGLINDLFGREDRLCEQTK---C 435
    ||:::||||:|:::|:::|:::|:::|:::|:::|
QY 470 YKVEYGVKRYMTVSGLEPPCIIHHRISCIHLALDMEIINGQ--VOYDGEVSQITIGITHEV 528
    ||:::||||:|:::|:::|:::|:::|:::|:::|
Db 436 EKISTLGDCTYCVAGCEPPEADHAYCCTEMEGAMIKALEQCEQKKEKVVNNRVGHTGV 495
    ||:::||||:|:::|:::|:::|:::|:::|:::|

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QY      529 VTGVIGQRMRYCLFQNTVNLSTRLETGGEKKNVSYTYRCLMSPENDPQCHLE 585
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      496 LCGILGMRPFKFDVMSNDVNLNLMEQLGVAGKVFHISATAKYL-----DDREME 546

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: RESULT 8
: US-08-894-173-2
: Sequence 2, Application US/08894173A
: Patent No. 6090612
:
: GENERAL INFORMATION:
:
: APPLICANT: Medical Research Council
: TITLE OF INVENTION: Adenylate cyclase and
: FILE REFERENCE: P14176C
: CURRENT APPLICATION NUMBER: US/08/894,173A
: CURRENT FILING DATE: 1997-08-13
: NUMBER OF SEQ. ID NOS: 97
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 2
:
: LENGTH: 1353
: TYPE: PRT
:
: ORGANISM: Mouse
:
: FEATURE:
:
: OTHER INFORMATION: HYPOTHETICAL : NO
:
: US-08-894-173-2

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Query Match	9.0%	Score 291.5;	DB 3.	Length 1353;
Best Local Similarity	31.28;	Pred. No. 1.3e-19;		
Matches 74;	Conservative 44;	Mismatches 72;		
			Indels 47;	Gaps 6

```

QY      383  LEDKKRTDLYLVLPSPVANEL-----RRK-----409
Db      323  LEVFKALKERKIHSMRPLINDLDMKQODESESNVKNHAISSPKNRKKSSIQAPLAF 382
QY      410  RPVEAKRYDNTVLTISGIVGFNAFCSKHASGEGAMKIVNLNDLYTRDFTLDSRKNPFV 469
Db      383  RPFKMOOIEEVSILEFADIVGF-----TKSANKSAHALVGLINDLFGRRDRLCEQKRC---C 435
QY      470  YKVEIVGDKVYTVSGGLPBPCCIHHARISCHLALDMMELNGQ-VQVDSGEVQITIGHTGEV 528
Db      436  EKISTLIDCCYCVAGCPEPRADHAYCCITEMELGMKALAEQCCQEKREKVMNHWGVTHTGV 495
QY      529  VTGIVGQRMPRYCLFEGNVNLTSRTEFTGEKGINVSEYTRCLMSPENSDPOFILE 585
Db      496  LCGILGMRREKFQVWMSNDVNLAMLEQGLCVAGKHAISATAKYL-----DDRYME 546

```

```

RESULT 9
US-09-398-193-2
: Sequence 2. Application US/09398193
: Patent No. 6197581
: GENERAL INFORMATION:
: APPLICANT: Medical Research Council
: TITLE OF INVENTION: Adenylate cyclase and uses therefor
: FILE REFERENCE: P24160-
: CURRENT APPLICATION NUMBER: US/09/398,193
: CURRENT FILING DATE: 1999-09-17
: NUMBER OF SEQ ID NOS: 104
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 2
: LENGTH: 1353
: TYPE: PRT
: ORGANSIM: Mouse
: FEATURE:
: OTHER INFORMATION: HYPOTHETICAL : NO
: US-09-398-193-2 .

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Query Match          9.0%: Score 291.5; DB 4; Length 1353;
Best Local Similarity 31.2%: Pred. NO. 1.3e-19;
Matches 74; Conservative 44; Mismatches 72; Indels 47; Gaps 6;

383 LEDEKKTDTLLIVSLPPSVANEL-----NKK-----409
|| || : : : || : : : ||

```

```

0Y      383 LEDEKKKTDLLSYLPPSVANEL-----RHK-----409
      || || : ::||:| :|::|

```


RESULT 12
US-08-726-214-6
Sequence 6, Application US/08726214
Patent No. 6107076
GENERAL INFORMATION:
APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,214
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSD:450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1144 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-726-214-6
Query Match
Best Local Similarity 8.9%; Score 286.5; DB 3; Length 1144;
Best Local Similarity 21.8%; Pred. No. 3.1e-19;
Matches 119; Conservative 104; Mismatches 201; Indels 121; Gaps 19;
QY 165 KVIQNRNECDHNOFLIEEKSEKEDFEEDLDREENGTOESRISPTTECKAPFHTIFD 224
DB 599 QVKKRNTFLIMKFMPEMETR---YSVEKESGAAFGSCCVVLFCTAM-VETLID 652
QY 225 -----RDVVTOCGNAIYRVLPOLP-----GNCGLS 252
DB 653 PWIMTYVTFVGEVLLILITICMA--AIFPRAFRKKVAFSSWIDRTMARTAMLA 710
QY 253 VESLVRPH-IDT-----SFGILSHINTVFLRSK 281
DB 711 IFILVANYVDMSCLOYWMPYNTTIGILDGCMENPKRYNVAVLSIATIMLVQ-- 768
QY 282 EGLDVEKCEDELTEISCLRLKGOMIYLPDADSIILFCSPVY---NDDDLFRG 337
DB 769 --VSHWKLTLMLLVGA-VTAIINLAWCPDEFEDYHRRFOEKDSPVVALEKQVSTPG 825
QY 338 LVLSD--IPLDARTDL-VLLGEQFREYKLTQELITLRLQTLALDEKKK----- 389
DB 826 LNTGDSRLPLVPKYSITVAMLSFYFSRHVEKATLTLMLKEVLDQEKERYEMR 885
QY 390 --TDTLISVLPSPVANEL---RHKRPYAKRYDVTILFSGIYGFNAFCRSKASGEA 443
DB 886 RRMNEALVTNMLPEHVARHFLGSKRDELSQSYDEIGVAFSLPNRADPTYESINNG 945
QY 444 MKIVNLNDLITRFDTLDSRKNPFYKYVETVGDKTMTVSGLPDPCIH----- 491

RESULT 13
US-09-398-193-99
Sequence 99, Application US/09398193
Patent No. 6197581
GENERAL INFORMATION:
APPLICANT: Medical Research Council
TITLE OF INVENTION: Adenylyl cyclase and uses therefor
FILE REFERENCE: P24360-
CURRENT APPLICATION NUMBER: US/09/398,193
CURRENT FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 104
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 99
LENGTH: 1353
TYPE: PRT
ORGANISM: Human
US-09-398-193-99
Query Match
Best Local Similarity 8.8%; Score 283.5; DB 4; Length 1353;
Best Local Similarity 30.8%; Pred. No. 8.2e-19;
Matches 73; Conservative 44; Mismatches 73; Indels 47; Gaps 6;
QY 383 LEDEKRTDTLYSVLPSPVANEL-----RHK----- 409
DB 323 LEVKAALKERHIMHSVPMRIIADLMDKGDESESNVYKRNATSSPKNNKKSIOKAPIN 382
QY 410 RPYPARRYDNTVTLFSGIYGFNAFCRSKASGEAMKIVNLNDLITRFDTLDSRKNPFY 469
DB 383 RPKMOOIEVYSILFADIVGF---TKMSANKSAHALVGLNLDLFGFRDLCEETK---C 435
QY 470 KYVEYGDKRYMTVSGLPDPCIHRSICHLALDMMETIAGO-VYVDGSEYVOTIGITGEV 528
DB 436 EKISTGDCYCYACGCEPADADHAYCCIEGLGHIKAIIDFQCEKKEAMNRYGVHITRY 495
QY 529 VTGVIGORMRYCLFGNTVNLTSRTETTGKGRINVSERYRCIMSPENDPOFHE 585
DB 496 ICGILGMRBRKFPVWSNDVNLMLMDQLGAVGVHISEAVAKYL-----DDRYEME 546
RESULT 14
US-08-726-214-14
Sequence 14, Application US/08726214
Patent No. 6107076
GENERAL INFORMATION:
APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/726,214
 FILING DATE: Concurrently Herewith
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/005,498
 FILING DATE: 04-OCT-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Highlander, Steven L.
 REGISTRATION NUMBER: 37,642
 REFERENCE/DOCKET NUMBER: UTSD:450
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEFAX: (512) 474-7577
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1099 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-726-214-14

Query Match 8.7%; Score 282.5; DB 3; Length 1099;
 Best Local Similarity 29.3%; Pred. No. 7.2e-19;
 Matches 84; Conservative 55; Mismatches 97; Indels 51; Gaps 9;

QY 334 TRRGILYLDIPDHATRLVLLGEOFFREY-----KTOELEITLRLQLTLRLLEDEK 387
 DB 176 TQLGQL-----LANAVILLGNGFTGAFHKLQDASRLFIYTVACIOIRRLRYEK 228
 QY 388 KKTDTLXSVLPSPVANEL-----RHKR-----VPKRYDVTILFSGIV 428
 DB 229 ROEENLLSVLPRIHSMKALITRLKEGDRHMPDNHSLYKRNQVSLIADIV 288
 QY 429 GFNAFCSKHAEGEGAMKIVNLNDLYTRFDLTDSRKNPFYKVTVDGKYMTVSGLPEP 488
 DB 289 GF-----TLASDCSPKELVYVNLFLGKFDQAKANE--CMRIKILGDCYCVSGLPVS 341
 QY 489 CIHARSTICHLADMETIAGOV-QYDGSVOITIGIHTEGYVTGYIGQMPRYCLFGNTV 547
 DB 342 LPTNARNCVKMGDLICEAIKQVREATGVDISMRVGHSGNYLCGVIGLRKQYDWSHDV 401
 QY 548 NUTSRTEFTGKINVSERYRCIMSPENDPOF-----HLEHRGP 589
 DB 402 SLANMEAGVPGRYHTEATLNL-----DKAYEVEDGHEGRDP 442

RESULT 15
 US-09-474-076-2
 Sequence 2, Application US/09474076
 Patent No. 6465237
 GENERAL INFORMATION:
 APPLICANT: Tomlinson, James E.
 APPLICANT: COR Therapeutics, Inc.
 TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
 TITLE OF INVENTION: CYCLASE
 FILE REFERENCE: 44481-5028-01-US
 CURRENT APPLICATION NUMBER: US/09/474,076
 CURRENT FILING DATE: 1999-12-12
 PRIOR APPLICATION NUMBER: PCT/US98/13694
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/070,904
 PRIOR FILING DATE: 1997-07-01
 PRIOR APPLICATION NUMBER: 08/886,550
 NUMBER OF SEQ ID NOS: 2
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 2
 LENGTH: 1168

TYPE: PRT
 ORGANISM: human type VI adenylyl cyclase
 US-09-474-076-2
 Query Match 8.7%; Score 282.5; DB 4; Length 1168;
 Best Local Similarity 26.6%; Pred. No. 8e-19;
 Matches 94; Conservative 61; Mismatches 126; Indels 73; Gaps 12;

QY 296 LVTREISCLRL-----KGMIVLPE--ADSIILCSPSVANLMDLTRGILYLDIPDH 346
 DB 262 LSGGLSTLHLILAMQNRGDAFLMKQGANVLLFCT----- 299
 QY 347 DATRLVLLGEOFFREYKLTQLELITDRLQLTLRLADEKKKTDLLYSVLPSPVANEL 406
 DB 300 ---NVIGICHTYPAFVSQRQAFQETRGVQARLH-LQHNROQRLLSLVLPQVAMEM 354
 QY 407 R-----HRRPVPARKRYDVTILFSGIVGFNPFCSKHAEGEGAMKIVNLNDLY 454
 DB 355 KEDITKKEDMMFHK--IYIQKHNVSTILFADIEGFTSLASQCT---AQELVMTLNELF 408
 QY 455 TRFDLTDSRKNPFYKVTVDGKYMTVSGLPEPCIHARSICHLADMETIAGOV-QYD 513
 DB 409 ARFDKLAEN--HCLRIKILGDCYCVSGLPEARADRAHCCVEKGVMIKIASIVREY 465
 QY 514 GESVOITIGIHTEGYVTGYIGQMPRYCLFGNTVNLTSRTETTGKGINVSEYTRCLM 573
 DB 466 GVNVMNRVGIHSGRVHCGVIGLRKQFDWVSNDVTLANMEAGRAGRITRATILQYLN 525
 QY 574 SPENDP-----QFHLH--RGVPMSKKKKKPMQVFLSRKNTGEE 613
 DB 526 GDYEVEPGRGGRNAYLKEOHITETLLIG-ASQKRKEKAMIAKLQRRRANSE 578

Search completed: June 27, 2003, 13:05:59
 Job time: 14.7678 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2003, 13:05:32 ; Search time 32.6287 Seconds

(Without alignments)
2080.112 Million cell updates/sec

Title: US-09-762-767a-4

Perfect score: 3231
Sequence: 1 MYGFVNAHLELVIRNTPPE.....QVFLSRKNTGETEKQDD 619

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 424699 seqs, 10964683 residues

Total number of hits satisfying chosen parameters: 424699

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PC1_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	789.5	24.4	690	9	US-10-205-823-162 Sequence 162, App
2	778	24.1	691	9	US-09-952-213D-2 Sequence 2, Appl
3	407.5	12.6	1073	10	US-09-819-249-2 Sequence 2, Appl
4	405.5	12.6	1073	9	US-10-157-031-18 Sequence 18, Appl
5	291.5	9.0	1294	12	US-10-071-223-2 Sequence 2, Appl
6	291.5	9.0	1353	10	US-09-751-100B-2 Sequence 2, Appl
7	291.5	9.0	1353	12	US-10-071-223-3 Sequence 3, Appl
8	289	8.9	1080	9	US-10-282-942-2 Sequence 2, Appl
9	283.5	8.8	1353	10	US-09-751-100B-99 Sequence 99, Appl
10	282.5	8.7	1168	9	US-10-201-000-2 Sequence 2, Appl
11	282.5	8.7	1168	10	US-09-750-240-11 Sequence 11, Appl
12	278.5	8.6	604	10	US-09-750-240-4 Sequence 4, Appl
13	278.5	8.6	1167	10	US-09-750-240-6 Sequence 6, Appl
14	278	8.6	1261	9	US-10-175-136-2 Sequence 2, Appl
15	269.5	8.3	257	9	US-09-989-442-95 Sequence 95, Appl
16	269.5	8.3	302	10	US-09-915-582-50 Sequence 50, Appl
17	269.5	8.3	1077	10	US-10-121-911-1 Sequence 1, Appl
18	265.5	8.2	1167	10	US-09-750-240-13 Sequence 13, Appl
19	264	8.2	241	9	US-09-764-868-794 Sequence 794, App

20	264	8.2	241	9	US-09-989-442-141 Sequence 141, App
21	259.5	8.0	855	10	US-09-925-297-811 Sequence 811, App
22	242	7.5	225	9	US-09-989-442-92 Sequence 92, Appl
23	234.5	7.3	311	10	US-09-925-297-515 Sequence 515, App
24	175.5	5.4	670	9	US-10-051-643-178 Sequence 178, App
25	175.5	5.4	670	9	US-09-880-505-178 Sequence 178, App
26	175.5	5.4	722	9	US-10-051-643-174 Sequence 174, App
27	175.5	5.4	722	9	US-09-880-505-174 Sequence 174, App
28	173	5.4	419	9	US-10-051-643-125 Sequence 125, App
29	173	5.4	419	9	US-09-880-505-125 Sequence 125, App
30	172.5	5.3	112	10	US-09-205-658-75 Sequence 75, Appl
31	172.5	5.3	112	10	US-09-844-353A-75 Sequence 75, Appl
32	149	4.6	107	10	US-09-205-658-76 Sequence 76, Appl
33	149	4.6	107	10	US-09-844-353A-76 Sequence 76, Appl
34	137.5	4.3	88	10	US-09-751-100B-62 Sequence 62, Appl
35	137	4.2	85	10	US-09-751-100B-59 Sequence 59, Appl
36	137	4.2	85	10	US-09-751-100B-60 Sequence 60, Appl
37	137	4.2	85	10	US-09-751-100B-61 Sequence 61, Appl
38	134.5	4.2	90	10	US-09-751-100B-49 Sequence 49, Appl
39	131.5	4.1	90	10	US-09-751-100B-48 Sequence 48, Appl
40	131	4.1	24	9	US-10-106-698-5238 Sequence 5238, Ap
41	131	4.1	85	10	US-09-751-100B-54 Sequence 54, Appl
42	131	4.1	85	10	US-09-751-100B-55 Sequence 55, Appl
43	131	4.1	85	10	US-09-751-100B-56 Sequence 56, Appl
44	131	4.1	85	10	US-09-751-100B-57 Sequence 57, Appl
45	131	4.1	85	10	US-09-751-100B-58 Sequence 58, Appl

ALIGNMENTS

RESULT 1
US-10-205-823-162
; Sequence 162, Application US/10205823
; Publication No. US20030108963A1
GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ganavarapu, Manjula
; APPLICANT: Goratcheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamalkar, Shubhangi
; APPLICANT: Monsey, Angela M.
; APPLICANT: Glat, Karen
; APPLICANT: Zhao, Xumel
; APPLICANT: Anderson, Dustin
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILE REFERENCE: MRI-044
CURRENT FILING DATE: 2002-07-25
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: US/10/205, 823
PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: 60/314, 356
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/325, 020
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/341, 746
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/362, 158
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 162
LENGTH: 690
TYPE: PRT
ORGANISM: Homo sapiens
US-10-205-823-162
Query Match 24.4%; Score 789.5; DB 9; Length 690;
Best Local Similarity 35.1%; Pred. No. 5.3e-60;

Matches	207; Conservative	96; Mismatches	219; Indels	67; Gaps	15;
Oy	30 QLBEGGFLVRIITDYDSTYDLVAASVYLNINAGEIL-QMGKMEFYCOESGDTTLR	88			
Dd	101 KIKESRKLEERDEFKRTIAEQVAAGVY-----EVKESIGEVEFYCYEED-ENTLIG	153			
Oy	89 VLGSNVREFLONIDL-----HDHLATITPGKRAPSFCTDAEKKGILHYHSREGIQ	143			
Dd	154 VVGGLKNQFNLMSFTLLQSSHCQAGKRGRLIEDSLICDKE-DFELHYIYFFPKRTS	212			
Oy	144 DIVIGITVYAAQOHGTEIDMKVIOQNEECDHTO-----FLIEKESKEEDFY	192			
Dd	213 LILPGLIIAAAHVLEYETEVEVSLM-----PCFHNDCSEFVNOPYLLYSVHKMSTKPS---	265			
Oy	193 EDLORFEENGTOESRISPYT-FCKAFPHIIFRDLVYVTCGNALRYRLPQLQ-PGNSL	250			
Dd	266 -----LSPSKQSSLIYPTSLPCKTFPHFMFDKMTLLQNGGIRLRNRDRFOGKPF	320			
Oy	251 LSVSLVRPHIDISEHGILSHINTVFLRSKEGLDVEKLCDELTGTEISCLTKGOM	310			
Dd	321 EEFYELLTPKINQFSPGIMTMNQFVVRVRMDNSVK-----SSRVMDLKQGM	370			
Oy	311 IYLPBADSILFLCSPSVANNDDLRRGYISDIPHDTRDLYLGEQFPREYKLTQLE	370			
Dd	371 IYVESSALFLPGSCVDRLDFEGRGLYLDIPHLNLRBYVLLGEQARADGKRRIG	430			
Oy	371 ILTVRLQTLRLAEKCKKTDLLYSVLRPPSANELRRKRPVAPKRYNTWILFSGYGF	430			
Dd	431 KLNATLEQAQALAEKKKTYDLCISIPCEVAQQLMGQVYQAKKFNVTMLPEDIYGF	490			
Oy	431 NAFGSAHSGECAKIVYLNLDLT7RPTDITDSKRNPFYVYVEYVGDKYMTVSGLPETCI	490			
Dd	491 TALSQCS-----PLQVYIMLALYTRFQOCGEID-----VYKRETIQDAYCVAAGGILHESD	543			
Oy	491 HHARSICHLADMEIAGV-OVDSQVQITGHTGEMVGVIGIORPRLCFENTVNL	549			
Dd	544 THAVDIALMLAKMELSDSEVMSPHREPIKMRIGLHSGSVFAGYGVKAPKICLFGNNVTL	603			
Oy	550 TSPRETTGKCKINVSERYVCL-----NSPENSDFQFLEHNG	588			
Dd	604 ANKFECSVPPRKINVSPTTYRLCLKDCPGFVETPPRSREBLPPNPFSEIIG	652			
RESULT 2					
US-09-952-213D-2					
: Sequence 2, Application US/09952213D					
: Publication No. US20030096240A1					
: GENERAL INFORMATION:					
: APPLICANT: MURAD, FERID					
: APPLICANT: SHARINA, IRAIDA G.					
: APPLICANT: KRUBENACKER, J. S.					
: APPLICANT: MARTIN, E.					
: TITLE OF INVENTION: GENOMIC ORGANIZATION OF MOUSE AND HUMAN SGC					
: FILE REFERENCE: USH:252US					
: CURRENT APPLICATION NUMBER: US/09/952, 213D					
: CURRENT FILING DATE: 2002-08-16					
: NUMBER OF SEQ ID NOS: 15					
: SOFTWARE: PatentIn Ver. 2.1					
: SEQ ID NO 2					
: LENGTH: 691					
: TYPE: PRT					
: ORGANISM: Mus musculus					
US-09-952-213D-2					
Query Match					
Best Local Similarity 24.1%; Score 778; DB 9; Length 691;					
Matches 213; Conservative 105; Mismatches 224; Indels 94; Gaps 20;					
Oy	9 LELLYIRNYGGEVMEWDDIKKEAQLDEBEGGFLVRIITDYDSSKRTVDIVAASKVYLNINAGEILQ	68			
Dd	89 LNLALQRLAKHKRIEENKSKSEKED-----LKKITIAEEA-----IAAGAPVALK-----D	134			
Oy	69 MFGKMEFYCOESGDTTLIRVLSGNVREFLONIDL-----HDHLATITPGKRAPSFRC	123			

```

Db      135 SLGELFKICYED -EHILGVVGGTFLKDFLNSFTSLKQSHOCGEARRGRLEDA51LDL 193
QY      124 DAEKRGKLIHYSEREGLODIVIGIKYVAQOIHGTEIDMKYIOQRNEC--DHTQFL 180
Db      194 DKDQ-DENLVYFFFRKRTALLPGIKMAAILVESHVESLMT---DPCFRSDCTERY 248
QY      181 -----IEEKSEKDEVEDLDREENGTOGESRISPYT-FCKAPFHIFPRDLVYVQ 231
Db      249 NOPYLLYSVHWKSTKPS-----LSPKCPSSLIYRPSLCKTPTPFHMDRLDIAITQ 300
QY      232 CGNAIYRVLPOLO-PONCSLSVSFLVRPHIDISFGHLSHINTVYFLRSKGLLDYERL 290
Db      301 LGNGIRRLRYNKRDFOGKPRFEFEFFELITPKINQTESGIMTLMNQEVIRYRBDNSVKR 359
QY      291 ECEDELJTGEISCLRLKGMVILPEADSLIFCSPVMNLDLTRGLTSDLPILMDAR 350
Db      360 -----SSRVMDLKGMITIVESSALIFGSPVDRLDEDTGGLTSLDIPHNALR 410
QY      351 DLVLLEGEFRREBYKLTQLEIITDRIQTLRALDEDEKKTDTLYLSVLPSPYANELRHR 410
Db      411 DVLIGEORADQDGLKRLKGLKATLEHQAQLAEERKKTVOULGISPFSEVAQOLMOQ 470
QY      411 PYPARRYDNVITLESIGYGFNAPFCSKHASEGAKIVNLINDYTRFDTLTSRKAPFY 470
Db      471 IVQARKFESEVITMLFEDIDYETFAICSCS---PLOYITMLNLYTFPDDOCGLD--Y 523
QY      471 KVEFYGDYKMTVSGPPEPCIHARSICHALDMMETAGOV-QVDSGSOITIGIHTEYV 529
Db      524 KVEITGDNAVCAVAGLHRESDTHAVOIALMALCMELSEINVMSPHGPIKRIQIHSGSVF 583
QY      530 TGVIGQMRPRYCLFSGNTVNLISRTETTGEEKINSEYIRCL-----MSPEND 579
Db      584 AGVGVKMPRYCLFENNVTLANKFESC5VPRKINVSPTYYRLKDCPGFVTPRSREELP 643
QY      580 POF-----HL-----EHRGPVSMKKGEKPEQOVF 603
Db      644 PNFPSDIDPGICHTFLDAYHHQGPNS-----KPMF 671

RESULT 3
US-09-819-249-2
Sequence 2, Application US/09819249
Patent No. US20010029019A1
GENERAL INFORMATION:
APPLICANT: Waldman, Scott A.
APPLICANT: Park, Jason
APPLICANT: Schulz, Stephanie
TITLE OF INVENTION: Compositions And Methods For Identifying And Targeting Cancer
TITLE OF INVENTION: Alimentary Canal Origin
FILE REFERENCE: TUD2412
CURRENT APPLICATION NUMBER: US/09/819,249
CURRENT FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 60/192,229
PRIOR FILING DATE: 2000-03-27
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 1073
TYPE: PRT
ORGANISM: Homo sapiens
US-09-819-249-2

Query Match      12.6%; Score 407.5; DB 10; Length 1073;
Best Local Similarity 22.6%; Pred. No. 26-26;
Matches 180; Conservative 117; Mismatches 274; Indels 225; Gaps 26;

QY      12 VIRNYGGEVWEDIDKEAQLDEEGQFLVRIYDSDSKTYVLAAAS-----KVLNLNAGEI 66
Db      245 VIMNGGEFLKTKGDAVADYIIVLDLFDNDQYLEDNVTAPDYMKNVYLVLISPGNS 304
QY      67 L-----QMGKMFVEVQE-----SGYD 84

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Db	305	LINSFSRNLSPTRKDFRLAIVNGILTVGHMUKIFLENEENITTPREFAHFRLNLEPGXD	364
QY	85	-----TLRLVGSVNFREFLONLALHHLATIIYGMARPSRCDAE-----	126
Db	365	GPVTLDDMGVDSTWMLLYTSDTKRYKVLITYPDHVNKTPYDMSPTFWKNSKLPNDI	424
QY	127	KGKG---LILHYSEREGLODIVIGIITVAQINGSTEIDMVIQOR	170
Db	425	TGRPOLIMIVFT---LTGAVALLLVALMLKRYKRDYELROCKWSHIPENITPLE	480
QY	171	NEECDHFOFLTE-----KSKEDFEYEDLDRFENGQOESR-----IS	209
Db	481	TNEINHSLKIDDDKRDPTIQLRQCKYVKKVILKDLKHNQNTFEKOKIETKLQID	540
QY	210	PYTCKAFPEPHIIFEDRLVYQCGNAIYRVLQPOLPGNCSLSVSLVRPHIDISFGII	269
Db	541	YTLTLKFYG-----TWKIDMIGFVIEYCERG--SLREVLNDITISYDGTEDWE	588
QY	270	SHIMVFLRSKEGILDVEKCEDELGTETSLCRKMGQMIYLP--ADSTL-----	320
Db	589	KRISLYDIANGMSTYLSHSSKTEVHGRLNST--NCVADSRVVKYIDFGCNSILPRKDIM	646
QY	321	---FLCSPVYNLDDLTRGLYLSLDPLHDAT-----RD-----	351
Db	647	TAPHLRANISQKGDVYSYGLIAGELIIRKETFTYLSCRDNNEKIFRYENSGMPRE	706
QY	352	---LVLLGEQFREERYKTOE-----LEILND	374
Db	707	DLFLETAKELELYLVKNCWEEDPEKRDPKCIETTLAKIFGLPHDQNEGMYTLIR	766
QY	375	RLQJLTRLLED-----EKKKTDTLXSVLPSPVANELRHRPPAKRYDNTIL	423
Db	767	RLQYSRNLLEHLVEERTOLYKAERBARLNLMLPLRVVKSILKEKGFEPLELYEVTII	826
QY	424	FSGIYGFNAFCSKHNSGEGAMKIVLNDLYRPFPLUDSRKNPFYKVEYGDXYMTYS	483
Db	827	FSDIVGFTTC-KYST---PMEVMDLNDIYKSFHDIVHND--YKVEITGDATWVAS	879
QY	484	GLPE-PCIIHARSICHLADMMEIAGQOVD--GESVOITIGIHGEVTVGIVGOMPR	539
Db	880	GLPRNGNRHAIIDAKMALELISFNGTPELEHLPLPIRIRIGVHSGPCACAGVGIKMR	939
QY	540	YCLFGNTVNLTSRETTGEEKGKINSEYTYRCLMSPENDPOFHLHNRGPVSKGKEPM	599
Db	940	YCLGDFVNTASRMESTGLPLRIHVSSTAIL--KRTCEQFLYEVRGBETYLKGNET	966
QY	600	QWFLSLRKNGTGEERK	615
Db	997	TYWL-----TGAKDOK	1007

```

: RESULT 4
: US-10-157-031-18
: Sequence 18, Application US/10157031
: Publication No. US20030108890A1
: GENERAL INFORMATION:
: APPLICANT: Baranova, A. V.
: APPLICANT: Yankovsky, N. K.
: APPLICANT: Kozlov, A. P.
: APPLICANT: Lobashev, A. V.
: APPLICANT: Krukovskaya, L. L.
: TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
: FILE REFERENCE: 2/60-103
: CURRENT APPLICATION NUMBER: US/10/157,031
: CURRENT FILING DATE: 2002-05-30
: NUMBER OF SEQ ID NOS: 415
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 18
: LENGTH: 1073
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-10-157-031-18

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[illegible]

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: RESULT 5
: US-10-071-223-2
: Sequence 2, Application US/10071223
: Patent No. US20020137174A1
: GENERAL INFORMATION:
: APPLICANT: Storm, Daniel R.
: APPLICANT: Hacker, Beth
: APPLICANT: Tomlinson, James E.
: APPLICANT: COR Therapeutics, Inc.
: TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
: TITLE OF INVENTION: CYCLASE
: FILE REFERENCE: 44481-5028-02-US
: CURRENT APPLICATION NUMBER: US/10/071,223
: CURRENT FILING DATE: 2002-02-11
: PRIOR APPLICATION NUMBER: 09/473,717
: PRIOR FILING DATE: 1999-12-29
: PRIOR APPLICATION NUMBER: PCT/US98/13541
: PRIOR FILING DATE: 1998-07-01
: PRIOR APPLICATION NUMBER: 60/098,559
: PRIOR FILING DATE: 1997-07-01
: PRIOR APPLICATION NUMBER: 08/886,440
: PRIOR FILING DATE: 1997-07-01
: NUMBER OF SEQ ID NOS: 3
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 1294
: TYPE: prt
: ORGANISM: human type IX adenylyl cyclase
: US-10-071-223-2

```

Query Match	9.0%	Score 291.5	DB 12	Length 1294
Best Local Similarity	31.2%	Pred. No. 3.5e-16		
Matches	74	Conservative	44	Mismatches 72
			Indels	47
			Gaps	6
OY	383	LEDEKKKTDLLYSVLPSPVANEL	-----RRK-----	409
		::: :		
DB	323	LEVERKALKERHIMSPRIADIDDKOGDSESESVKRRHATSPKRRKKSSIOKAPIAF		382
OY	410	RPVAPKRRDNTYILFSGYGFNAFCSKHAASGGCAKLYNLNDLTTRPTLTDSKRNPV		469
		::: :	::: :	
DB	383	RPFKMQQILEEYSILFADIVGF---TKMSANKSAHALVGLNLDGREGREPLCEETK---C		435
OY	470	YKVEYGVGYKMTVSGLPSPCIIHARSICHLALDMEIINGQ-VQYDGESEQITIGITHGEV		528
		::: :	::: :	
DB	436	EKISITLGCYCYVACACPEPRADHATCCIEMLGAKIKALIQFOQEKKEKNNKMYGVATHGV		495
OY	529	VTGVIGQMPRYCCTGNTVNLTSRTETTGEGKRIWSEYTYRCLMSPENDSPQFIHE		585

Db 496 LCGILGMRKREKFDVMSNDVNLNLMEDLGAVGKHISEATAKYL-----DDRYEME 546

RESULT 6

US-09-751-1008-2

Sequence 2, Application US/097511008

Patent No. US20020142436A1

GENERAL INFORMATION:

APPLICANT: Medical Research Council

TITLE OF INVENTION: Human Adenylate Cyclase and Use Therefor

FILE REFERENCE: P27948A

CURRENT APPLICATION NUMBER: US/09/751,1008

CURRENT FILING DATE: 2000-12-28

NUMBER OF SEQ ID NOS: 104

SOFTWARE: PatentIn version 3.1

SEQ ID NO 2

LENGTH: 1353

TYPE: PRT

ORGANISM: Mouse

US-09-751-1008-2

Query Match 9.0%; Score 291.5; DB 10; Length 1353;

Best Local Similarity 31.2%; Pred. No. 3.7e-16;

Matches 74; Conservative 44; Mismatches 72; Indels 47; Gaps 6;

QY 383 LEDERKKTDTLLYSVLPPSVANEL-----RHK----- 409

Db 323 LEVERKALKERIMHSVMPRIIADLMKOGDESENSVSRHATSSPKNRKKSSIOKAPIAF 382

QY 410 RPVAKRYDNTILFSGVGNFACSKHASEGAMKIVNLLNDLYTRDTLDSRKNPV 469

Db 383 RPFMOQIEVSIILFADIVG-----TKMSANKSAHALVGLNDLFGFRDLCEQTK---C 435

QY 470 YKVEIVGDKYMTVSGLEPDCIHARSICHLALDMMETIAGQ-VQYDGESVOITIGIHGEV 528

Db 436 EKISTLDCCYCVAGCEPRADHAYCCIEMLGMIKALIEQPCQKEKENVNRVGHGTIV 495

QY 529 VTGVIGORMPRYCLFGVTNLTSTRTETGEGKINVSERYTRCLMSPENSDPQFHE 585

Db 496 LCGILGMRKREKFDVMSNDVNLNLMEDLGAVGKHISEATAKYL-----DDRYEME 546

RESULT 7

US-10-071-223-3

Sequence 3, Application US/10071223

Patent No. US20020137174A1

GENERAL INFORMATION:

APPLICANT: Storm, Daniel R.

APPLICANT: Hacker, Beth

APPLICANT: Tomlinson, James E.

APPLICANT: Cor Therapeutics, Inc.

TITLE OF INVENTION: Cloning and Characterization of a Human Adenylate Cyclase

FILE REFERENCE: 44481-5029-02-US

CURRENT APPLICATION NUMBER: US/10/071,223

CURRENT FILING DATE: 2002-02-11

PRIOR APPLICATION NUMBER: 09/473,717

PRIOR FILING DATE: 1999-12-29

PRIOR APPLICATION NUMBER: PCT/US98/13541

PRIOR FILING DATE: 1998-07-01

PRIOR APPLICATION NUMBER: 60/098,559

PRIOR FILING DATE: 1997-07-01

PRIOR APPLICATION NUMBER: 08/886,440

PRIOR FILING DATE: 1997-07-01

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3

LENGTH: 1353

TYPE: PRT

ORGANISM: murine type IX adenyl cyclase

US-10-071-223-3

Query Match 9.0%; Score 291.5; DB 12; Length 1353;

Best Local Similarity 31.2%; Pred. No. 3.7e-16;

Matches 74; Conservative 44; Mismatches 72; Indels 47; Gaps 6;

QY 383 LEDERKKTDTLLYSVLPPSVANEL-----RHK----- 409

Db 323 LEVERKALKERIMHSVMPRIIADLMKOGDESENSVSRHATSSPKNRKKSSIOKAPIAF 382

QY 410 RPVAKRYDNTILFSGVGNFACSKHASEGAMKIVNLLNDLYTRDTLDSRKNPV 469

Db 383 RPFMOQIEVSIILFADIVG-----TKMSANKSAHALVGLNDLFGFRDLCEQTK---C 435

QY 470 YKVEIVGDKYMTVSGLEPDCIHARSICHLALDMMETIAGQ-VQYDGESVOITIGIHGEV 528

Db 436 EKISTLDCCYCVAGCEPRADHAYCCIEMLGMIKALIEQPCQKEKENVNRVGHGTIV 495

QY 529 VTGVIGORMPRYCLFGVTNLTSTRTETGEGKINVSERYTRCLMSPENSDPQFHE 585

Db 496 LCGILGMRKREKFDVMSNDVNLNLMEDLGAVGKHISEATAKYL-----DDRYEME 546

RESULT 8

US-10-282-942-2

Sequence 2, Application US/10282942

Publication No. US20030087295A1

GENERAL INFORMATION:

APPLICANT: Sllas-Santiago, Immaculada

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE

FILE REFERENCE: WFO1-240PIRA

CURRENT APPLICATION NUMBER: US/10/282,942

PRIOR FILING DATE: 2002-10-29

PRIOR APPLICATION NUMBER: 60/335,047

NUMBER OF SEQ ID NOS: 2

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 1080

TYPE: PRT

ORGANISM: Homo sapien

US-10-282-942-2

Query Match 8.9%; Score 289; DB 9; Length 1080;

Best Local Similarity 26.3%; Pred. No. 4.4e-16;

Matches 94; Conservative 66; Mismatches 109; Indels 88; Gaps 12;

QY 236 IYRYLPQLOPNCGLSVFSLVRPHIDISFGLISHINTFYLSKRGGLDVERKBEDE 295

Db 136 VYTLPPSMRGAVAV-----GAVSTASHLLVLSLNG----- 167

QY 296 LTGTEISCLRLKGMVILPEADSLFLCSPSVNLDLTKRGYLSIDPLHATRDVLVL 355

Db 168 --GFTTSPVVRGLQL-----ANAVIFLCG-----NLGAFKH-----QMGDSRDL--- 208

QY 356 GEQPREKTLQELIETLDRQLTLRLADEKKTDTLLYSVLPVSA-----N 404

Db 209 -----FTYVVKCQIOIR-----RKIRIEKROEMILLVLPAAHISMCKALIIERLK 254

QY 405 ELRHRKRPV-----AKRYDNTILFSGVGNFACSKHASEGAMKIVNLLNDLYTR 456

Db 255 EHGDRKCPDNNFHSVLYKRNQNSVILYADIVGTOLASDQSPRE-----LVVYLNELFGK 310

QY 457 FDTLDSRKNPVYKVTGVGDKYMTVSGLEPDCIHARSICHLALDMMETIAGQ-VQDGE 515

Db 311 FDOJAKANE---CHRITLDCYCVAGSLVSLPTHARNCYKMGDLMOQAIKQVREKATGV 367

QY 516 SVQITIGIHGEVVTGVIGORMPRYCLFGVTNLTSTRTETGEGKINVSERYTRCL 572

Db 368 DINNRVGHSGNVLCVIGLKRKQYDVMSHDVSLANMEAGVGRVHTEATLKLH 424

RESULT 9

```

US-09-751-100B-99
; Sequence 99, Application US/09751100B
; Patent No. US20020142436A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: Human Adenylylate Cyclase and Use Therefor
; FILE REFERENCE: P27948A
; CURRENT APPLICATION NUMBER: US/09/751,100B
; CURRENT FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 99
; LENGTH: 1353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-751-100B-99

Query Match
Best Local Similarity 30.8%; Score 283.5; DB 10; Length 1353;
Matches 73; Conservative 44; Mismatches 73; Indels 47; Gaps 6

OY 383 LEDEKKKTDLLYSVLPSPVANEL-----RHK-----409
Db 323 LEVEALKERHHSVMPRIADDDLKKQDESESVKRAHATSSPKRKKSSIQAKPIAF 382
OY 410 RVPKARYDNTYILFSGIVGENAFCSKHAEGGAKIYNLNDLYTRDTLDSRRNPV 469
Db 383 RPFKQQLIEEVSILEADIVGF-----TKMSANKSAHALVGLNDLPGRFDRICEETK---C 435
OY 470 YKVENYGGKMTVSGSLPEPCIHHAISICHLADMEIAGQ-VQYDGEVQYITIGIHTEY 528
Db 436 EKISTLGGCYCVACGPEPRDHAHYCCITEMGKMTKALEQFCOEKKEKMMVMGVHTRTV 495
OY 529 VTGVIGQMPRYCIEGNTFVNLTSPRETTGEGKINVSERYTQCLMSPENDQPHLE 585
Db 496 LGGILGMRRFEDWMSNDVYNLANLMEQGVAGKHAISEATAYL-----DRIYEME 546

RESULT 10
US-10-201-000-2
; Sequence 2, Application US/10201000
; Publication No. US20020187540A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, James E.
; APPLICANT: COR Therapeutics, Inc.
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
; TITLE OF INVENTION: CYCLASE
; FILE REFERENCE: 44481-5028-01-US
; CURRENT APPLICATION NUMBER: US/10/201,000
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US/09/474,076
; PRIOR FILING DATE: 1999-12-12
; PRIOR APPLICATION NUMBER: PCT/US98/13694
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/070,904
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/886,550
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1168
; TYPE: PRT
; ORGANISM: human type VI adenylyl cyclase
US-10-201-000-2

Query Match
Best Local Similarity 26.6%; Score 282.5; DB 9; Length 1168;
Matches 94; Conservative 61; Mismatches 126; Indels 73; Gaps 12

OY 296 LTGTEISCLRL-----KGMIVLPE-ADSIIIFGSPSVNWNDDLDRRGILSDIPHL 346
Db 262 LSGIGLSTLHILITAMQLNRGAFLMKQCGANVLEFLCT-----299

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QY      347  ATGTTTGGCGFRRREKYLTOLELTIDTRLOUTLALDEKKKDTLLYSVPSPVANEL 406
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QY      407  R-----HKRPVPAKRVDNVTLLFSGTIVFNACSKHASGEGAMKIYNLTNDLY 454
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QY      455  TRFDPLDLSRKNPFYKYVEYWGDKWTWYSGLDPEPCIIHARSICHLALDMETAGOV-QVD 513
Db      409  ARFDLALEN---HCRLRIKLGDCCYYCVSGSIPEARADNAHCCEVGVMIEAISLVREYT 465
QY      514  GESVOITLIHGTEVTVGIQGBMRPYCLFGFTVLNLSTETETGEKGINSEYTYRCIM 573
Db      466  GVNMMRVGHSHGRVCHGVGLGRKMQFDVMSNDVTLANMEGGARGRHITRAVLQYLIN 525
QY      574  SPENDP-----OFLEH---KGPSMKGKKPEMOWFLSRKNTGEE 613
Db      526  GDYEPEPRGERGNAYLMKHQHEFTPLLIG-ASQRKEEKAKMLAKIQIRANSME 578

RESULT 11
US-09-750-240-11
; Sequence 11, Application US/09750240
; Patent No. US20020103147A1
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; TITLE OF INVENTION: FAILURE
; FILE REFERENCE: 220002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-750-240-11

Query Match          8.7%; Score 282.5; DB 10; Length 1168;
Best Local Similarity 26.6%; Pred. No. 1,8e-15;
Matches    94; Conservative   61; Mismatches 126; Indels   73; Gaps   12

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PRIOR APPLICATION NUMBER:	60/246,475
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PRIOR FILING DATE:	2000-09-08
PRIOR APPLICATION NUMBER:	60/233,055
PRIOR FILING DATE:	2000-09-14

Query Match	8.3%	Score 269.5;	DB 9;	length 257;
Best Local Similarity	29.6%	Pred. NO. 2.4e-15;		
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Db 61 OSCECAVAMFASIANSEFYVELLEANNEGVECLRLNELIADFPBIEISDRFRLERIKT 124
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Db 233 CRXVYKVGKGE- - -MNTYFLN 251

Search completed: June 27, 2003, 13:17:13
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